

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 6, 2001, 08:29:41 ; Search time 13876.8 Seconds
(without alignments)
12066.075 Million cell updates/sec

Title: US-09-497-957-3
Perfect score: 10825
Sequence: 1 TCTAAGGTTGAGATAAAATT.....TCCCCAAATTTTCATAAAC 10825

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues 2688314
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba1.*
2: gb_ba2.*
3: gb_ba3.*
4: gb_in1.*
5: gb_in2.*
6: gb_in3.*
7: gb_om.*
8: gb_ov.*
9: gb_pat1.*
10: gb_pat2.*
11: gb_ph.*
12: gb_pl1.*
13: gb_pl2.*
14: gb_pl3.*
15: gb_pl4.*
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18: em_fun.*
19: em_htgo_hum.*
20: em_htgo_inv.*
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22: em_htg_hum1.*
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96: gb_vil2.*
97: gb_vil2.*
98: em_ba3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	10823.4	100.0	246240	9	AR036572 Sequence
2	10823.4	100.0	246240	9	AR036573 Sequence
3	10823.4	100.0	246240	9	AR036574 Sequence
4	10760.2	99.4	12146	93	HSHE
C 5	10659	98.5	193752	80	AL359892 Homo sapi
C 6	7542.4	69.7	246282	97	HSU91328
7	4251	39.3	101099	90	AL353759 Human hered
8	1421	13.1	1479	93	HSHLAA6

	9	1407.4	13.0	4349	7	AF301592	b
	10	1051.6	9.7	2727	97	HSU060319	AF0319 Homo sapien
	11	1030.2	9.5	1885	89	AF144242	Homo sapi
	12	832.2	7.7	874	93	SHSLAH4	Y09800 H.sapiens H
	13	768.8	7.1	772	89	AF184234	Homo sapi
	14	740.2	6.8	3334	7	AF301591	AF301591 Ceratother
	15	677.8	6.3	794	89	AF144238	Homo sapi
	16	657	6.1	761	93	SHSLAH1	Y09801 H.sapiens H
	17	637.8	5.9	653	93	SHSLAH4	Y09803 H.sapiens H
	18	547	5.1	547	89	AF147392	Homo sapi
	19	546.2	5.0	551	89	AF331065	Homo sapi
	20	517	4.8	517	10	I82158	Sequence 4
	21	516	4.8	517	10	I82167	Sequence 13
	22	515.4	4.8	517	10	I82157	Sequence 3
	23	511.6	4.7	526	93	SHSLAH7	Y09802 H.sapiens H
	24	429.6	4.0	987	89	AF150664	Homo sapi
c	25	398.2	3.7	128915	78	AL136458	Homo sapi
	26	394.2	3.6	182866	79	AL162739	Homo sapi
	27	393.8	3.6	103259	62	AC012430	Homo sapi
	28	389	3.6	190112	83	AP002354	Homo sapi
c	29	388.6	3.6	203361	78	AL139338	Homo sapi
c	30	386.4	3.6	97065	82	AP000768	Homo sapi
c	31	386.2	3.6	203986	77	AC087501	Homo sapi
c	32	383.2	3.5	178483	77	AC087238	Homo sapi
c	33	382.6	3.5	230917	67	AC022884	Homo sapi
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c	37	381	3.5	169947	67	AC022279	Homo sapi
c	38	380.8	3.5	183334	87	AC020558	Homo sapi
c	39	380.6	3.5	171811	77	AC084801	Homo sapi
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c	41	378.8	3.5	160169	72	AC051664	Homo sapi
c	42	377.6	3.5	678	89	AF144245	Homo sapi
c	43	377.2	3.5	105787	87	AC010458	Homo sapi
c	44	376.2	3.5	154471	67	AC022523	Homo sapi
c	45	376	3.5	173071	87	AC009477	Homo sapi

ALIGNMENTS

RESULT	1	PAT	29-SEP-1999
LOCUS	AR036572	DNA	
DEFINITION	Sequence 20 from patent US 5872237.		
ACCESSION	AR036572		
VERSION	AR036572.1	GI:5953240	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 246240)		
AUTHORS	Feder,J.Nathan, Kromal,G.Scott, Lauer,P.M., Ruddy,D.A., Thomas,W.		
TITLE	Tsuchihashi,Z. and Wolff,R.K.		
JOURNAL	Megabase transcript map: novel sequences and antibodies thereto		
FEATURES	Patent: US 5872237-A 20 16-FEB-1999;		
source	Location/Qualifiers		
	1..246240		
	/organism="unknown"		
BASE COUNT	73211 a 50177 c 50599 g 72252 t	1 others	
ORIGIN			

Query Match	100.0%;	Score 10823.4;	DB 9;	Length 246240;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 10824;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps

Qy	1	TCTAAGGTCAGATAAAATTTTAAATCATCATGATTGAATTTTGAAATCATAAATATTATTA	60
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Qy	61	AATATCTAAAGTTTCAGATCAGAACACTTCGCAGAGCTACTTTCCCAATCAACAACACCCT	120

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Db 193504 TAATGAACATGTAAGCAATGACACTCACTCTTAAGTTTACATCTCATATCTGATCTTAATTGA 193563
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QY 1321 GGAATTCAGATTATATACTCTTTTCAAGTTTACAAGAACAATAAATAAATCTGGTTTCTG 1380
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Db 193684 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTATAGTTGACAGTAGTATTTGCCCTGTAG 193743
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Db 193984 AAATATTCATGTTTACAAAGTGAATAGTCCAGCCATGTGTTGCATGTTTCAAGCCC 194043
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Db 194284 TTGGATTAAGGACGGGTTTTCTCAGCACTACTCATGTTGTGTGTGGGGGGGGGG 194343
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Db 194344 CGGCGTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGCTAGCAGTATCCCTGT 194403
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QY 2161 AAATTTGGCCATGTCACCTAGTAGCAAACTCTCTGGTTAAGAACTCGGGTTGAAGA 2220
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QY 2401 AAGGGAGCAACAGTAATAAGCAGGAGCCAGCCAGGAAGCTGTACACAGTCCAGGCAG 2460
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QY 2461 AGGTAGTGGAGTGGCTGGGTGGGAACAAGAAAGGAGTGACAAACCATTTGCTCTCTGAA 2520
Db 194764 AGGTAGTGGAGTGGCTGGGTGGGAACAAGAAAGGAGTGACAAACCATTTGCTCTCTGAA 194823
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QY 6181 TAGTACCTCTGCCCCAGGACAGTGGGAAGAGGGGAGAGGGATCTGGCATCCATGGG 6240
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QY 6301 AATGGTTCTCCCAAGTGAAGTCTCTAATTCAACAAACATCTTCAGAGCACCTACTAT 6360
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QY 6661 GAGTATAAGGCATACTGGAGATTAGAAATAATTACTGTACCTTAACCCCTGAGTTGCGT 6720
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QY 6781 GAATCAGAAAGACCCAGCTCATACAGAGTCCCAAGGCTCTTTTGGGATATTGGTTATGA 6840
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QY 7501 CTTACATGATTTTAACTCTGAGAAAGCTTGAACCTGGGAGCTGGCTAGTCTAT 7560
Db 199804 CTTACATGATTTTAACTCTGAGAAAGCTTGAACCTGGGAGCTGGCTAGTCTAT 199863
QY 7561 AACCTTACAGATTTTACACATGATCTATGCAATTTTCTGGACCCCTTCAACTTTTCCT 7620
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QY 7681 CATCTGATTTGATGTGAGTTGACAGCTATGAAGGCTGTACACTGCACGAATGGGAAG 7740
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RESULT 2
AR036573 AR036573 246240 bp DNA PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 21 from patent US 5872237.
ACCESSION AR036573
VERSION AR036573.1 GI:5953241
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
UnClassified.

REFERENCE 1 (bases 1 to 246240)
AUTHORS Feder,J.Nathan, Kronmal,G.Scott, Lauer,P.M., Ruddy,D.A., Thomas,W.,
Tsuchihashi,Z. and Wolff,R.K.
TITLE Megabase transcript map: novel sequences and antibodies thereto
JOURNAL Patent: US 5872237-A 21 16-FEB-1999;
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1. 246240
BASE COUNT 73211 a 50177 c 50599 g 72252 t 1 others
ORIGIN
Query Match 100.0%; Score 10823.4; DB 9; Length 246240;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10824; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 199864 AACCTTACCAGATTTTACACATGATCTATGCAATTTTCTGGAGCCCTTCAACTTTTCC 199923
Qy 7621 TTGAATCCCTCTCTGTTTACCAGTAACCTATCTGTCACCAAGCCCTTGGGATTTCTC 7680
Db 199924 TTGAATCCCTCTCTGTTTACCAGTAACCTATCTGTCACCAAGCCCTTGGGATTTCTC 199983
Qy 7681 CATCTGATTTGTGATGTGAGTTGCACAGCTATGAAGCTGTACACTGCACGAATGGAAGAG 7740
Db 199984 CATCTGATTTGTGATGTGAGTTGCACAGCTATGAAGCTGTACACTGCACGAATGGAAGAG 200043
Qy 7741 GCACCTGTCCAGAAAAGCATCATGCTATCTGTGGGTAGTAGTGGTGTATTTAGC 7800
Db 200044 GCACCTGTCCAGAAAAGCATCATGCTATCTGTGGGTAGTAGTGGTGTATTTAGC 200103
Qy 7801 AGGTAGGAGGCAATATCTTGAAAGGGTGTGAAGAGGTGTTTTTCTAATTTGGCATGA 7860
Db 200104 AGGTAGGAGGCAATATCTTGAAAGGGTGTGAAGAGGTGTTTTTCTAATTTGGCATGA 200163
Qy 7861 AGGTGTCATACAGATTTGCAAGTTTAAATGTGCTTCAATTTGGGATGCTACTAGTAT 7920
Db 200164 AGGTGTCATACAGATTTGCAAGTTTAAATGTGCTTCAATTTGGGATGCTACTAGTAT 200223
Qy 7921 TCCAGACCTGAAGATCACAATAATTTTCTACCTGGTCTCCTTGTCTGATATGAATGAA 7980
Db 200224 TCCAGACCTGAAGATCACAATAATTTTCTACCTGGTCTCCTTGTCTGATATGAATGAA 200283
Qy 7981 ATTATGATAAGGATGATAAAGCACTTACTTCTGCTCCGACTCTTCTGAGCACTACTTA 8040
Db 200284 ATTATGATAAGGATGATAAAGCACTTACTTCTGCTCCGACTCTTCTGAGCACTACTTA 200343
Qy 8041 CATGCAATCTGATGCACTTCTTACAATAATTTCTATGAGATAGTACTATATCCCAT 8100
Db 200344 CATGCAATCTGATGCACTTCTTACAATAATTTCTATGAGATAGTACTATATCCCAT 200403
Qy 8101 TTTCTTTTTTAAATGAAGAAAGTGAAGTAGCGCGGACGGTGGCTCAGCCCTGTAATCCC 8160
Db 200404 TTTCTTTTTTAAATGAAGAAAGTGAAGTAGCGCGGACGGTGGCTCAGCCCTGTAATCCC 200463
Qy 8161 AGCACTTTGGGAGGCCAAAGCGGGTGGATCATCGAGGTCAGGAGATCGAGACCATCTGGC 8220
Db 200464 AGCACTTTGGGAGGCCAAAGCGGGTGGATCATCGAGGTCAGGAGATCGAGACCATCTGGC 200523

Qy 8221 TAACATGGTGAACCCCATCTCTAATAAAAAATACAAAAATTAGCTGGCCTGGTGGCAG 8280
Db 200524 TAACATGGTGAACCCCATCTCTAATAAAAAATACAAAAATTAGCTGGCCTGGTGGCAG 200583
Qy 8281 ACGCCTGTAGTCCCAGCTACTCGGAAGGCTGAGCAGGAGAAATGGCAATGAACCCAGGAG 8340
Db 200584 ACGCCTGTAGTCCCAGCTACTCGGAAGGCTGAGCAGGAGAAATGGCAATGAACCCAGGAG 200643
Qy 8341 CAGAGCTTGCAGTGAGCCGAGTTTGGCCACTGCACCTCCAGCTAGGTGACAGAGTGAGA 8400
Db 200644 CAGAGCTTGCAGTGAGCCGAGTTTGGCCACTGCACCTCCAGCTAGGTGACAGAGTGAGA 200703
Qy 8401 CTCCATCTCAAAAAATAAAAATAAAAATAAAAATAAAAATAAAAATAAAAATAAAAAT 8460
Db 200704 CTCCATCTCAAAAAATAAAAATAAAAATAAAAATAAAAATAAAAATAAAAATAAAAAT 200763
Qy 8461 TAGAGTATCTCATAGTTTGTCTAGTGATAGAAACAGAGTTTCAAACTCAGTCAATCTGACCG 8520
Db 200764 TAGAGTATCTCATAGTTTGTCTAGTGATAGAAACAGAGTTTCAAACTCAGTCAATCTGACCG 200823
Qy 8521 TTTGTATACATCTCAGACACCACTACATTCAGTAGTTTGTAGTCCCTAGATAATTAATAGAGAA 8580
Db 200824 TTTGTATACATCTCAGACACCACTACATTCAGTAGTTTGTAGTCCCTAGATAATTAATAGAGAA 200883
Qy 8581 GGAAGGAGATGGCTCTCTTCTTGTCTCATTTGTCTTCTCTGAGTGAGCTTGAATCAGAT 8640
Db 200884 GGAAGGAGATGGCTCTCTTCTTGTCTCATTTGTCTTCTCTGAGTGAGCTTGAATCAGAT 200943
Qy 8641 GAAGGGAAACAGAGAAAACCAACCACTCATCTCAGCTGTCTATGTTCTCTTTTAAAGTC 8700
Db 200944 GAAGGGAAACAGAGAAAACCAACCACTCATCTCAGCTGTCTATGTTCTCTTTTAAAGTC 201003
Qy 8701 CTTGAAGGAGGTCCTCGAATGTGACTCCCTGCTCTCTGTTGCTCTCTTTGGCATTTCA 8760
Db 201004 CTTGAAGGAGGTCCTCGAATGTGACTCCCTGCTCTCTGTTGCTCTCTTTGGCATTTCA 201063
Qy 8761 TTTCTTTGGACCTCAGCAAGGACTGTAATTTGGTGGGACAGCTAGTGGCCCTGCTGGGC 8820
Db 201064 TTTCTTTGGACCTCAGCAAGGACTGTAATTTGGTGGGACAGCTAGTGGCCCTGCTGGGC 201123
Qy 8821 TTCACACAGGTCCTCTCCCTAGGCCAGTCCCTCTGAGCTCAGAACTCTGTTGGTATTTTC 8880
Db 201124 TTCACACAGGTCCTCTCCCTAGGCCAGTCCCTCTGAGCTCAGAACTCTGTTGGTATTTTC 201183
Qy 8881 CCTCAATGAAGTGGAGTAAAGCTCTCTCATTTTGTAGATGATATAATGGAAGCACCAGTG 8940
Db 201184 CCTCAATGAAGTGGAGTAAAGCTCTCTCATTTTGTAGATGATATAATGGAAGCACCAGTG 201243
Qy 8941 GCTTAGAGGATGCCAGGTCCTTCCATGGAGCCACTGGGTTCCCGTGACATTAATAAAA 9000
Db 201244 GCTTAGAGGATGCCAGGTCCTTCCATGGAGCCACTGGGTTCCCGTGACATTAATAAAA 201303
Qy 9001 AAAATCTAACCCAGGACATTCAGGAATTTGTAGATTTCTGGGAAATCAGTTTCACCATGTTCA 9060
Db 201304 AAAATCTAACCCAGGACATTCAGGAATTTGTAGATTTCTGGGAAATCAGTTTCACCATGTTCA 201363
Qy 9061 AAGAGTCTTTTTTTTTTTTTTTTGTGAGACTCTATTGGCCAGCTGGAGTGCAATGGCATGAT 9120
Db 201364 AAGAGTCTTTTTTTTTTTTTTTTTTGTGAGACTCTATTGGCCAGCTGGAGTGCAATGGCATGAT 201423
Qy 9121 CTCGGCTCAGCTGAACCTCTGCTCCAGGTTTCAAGGATTCCTCTGCTCAGCCCTCCCA 9180
Db 201424 CTCGGCTCAGCTGAACCTCTGCTCCAGGTTTCAAGGATTCCTCTGCTCAGCCCTCCCA 201483
Qy 9181 AGTAGCTGGGATTTACAGGCTGCACCACCATGCCCCGGCTAAATTTTTTGTATTTTTTAGTAGA 9240
Db 201484 AGTAGCTGGGATTTACAGGCTGCACCACCATGCCCCGGCTAAATTTTTTGTATTTTTTAGTAGA 201543
Qy 9241 GACAGGTTTTCACCATGTTGGCCAGGCTGGTCTGCACTCTCTGACCTCGTGATCCGCC 9300
Db 201544 GACAGGTTTTCACCATGTTGGCCAGGCTGGTCTGCACTCTCTGACCTCGTGATCCGCC 201603

QY	9301	TGCGTCGGCCCTCCCAAGATGCTGTAGATTACAGTGTGAGCACCCTGCCAGCGGTCFAAA	9360
Db	201604	TT	
		TGCGTCGGCCCTCCCAAGATGCTGTAGATTACAGTGTGAGCACCCTGCCAGCGGTCFAA	
QY	9361	AGAGTCCTTAATATATATATATCCAGATGCGCATGTCTTTACTTTATTTGTTTACTACATGACACTTG	9420
Db	201664	AGAGTCCTTAATATATATATATCCAGATGCGCATGTCTTTACTTTATTTGTTTACTACATGACACTTG	201723
QY	9421	GCTGCATAAATGTGGTACAAGCAATCTGTCTTGAAGCGCAGGTGCTTCCAGGATACCATAT	9480
Db	201724	GCTGCATAAATGTGGTACAAGCAATCTGTCTTGAAGCGCAGGTGCTTCCAGGATACCATAT	201783
QY	9481	ACAGCTCAGAAGTTTCTTCTTTTAGGCAATTAATTTTAGCAAGATATCATCTCTCTTT	9540
Db	201784	ACAGCTCAGAAGTTTCTTCTTTTAGGCAATTAATTTTAGCAAGATATCATCTCTCTTT	201843
QY	9541	TTAAACCATTTTCTTTTTTTTGTGGTTAGAAAAGCTTATGTAGAAAAAGTAAATGTGATTT	9600
Db	201844	TTAAACCATTTTCTTTTTTTTGTGGTTAGAAAAGCTTATGTAGAAAAAGTAAATGTGATTT	201903
QY	9601	ACGCTCAATGTAGAAAAGCTPATAAAAATGAATACAAATTAAGCTGTGTTATTTAATTAGCCAG	9660
Db	201904	ACGCTCAATGTAGAAAAGCTPATAAAAATGAATACAAATTAAGCTGTGTTATTTAATTAGCCAG	201963
QY	9661	TGA AAAACTATTAACAAC TTGTCTATTAACCTGTTAGTATTATTGTGCAATTA AAAATGCA	9720
Db	201964	TGA AAAACTATTAACAAC TTGTCTATTAACCTGTTAGTATTATTGTGCAATTA AAAATGCA	202023
QY	9721	TAT ACTTTTAATAATGTATAT TGTATTGTATCTGCATGATTTATTTAGAGTTCTTGTTTC	9780
Db	202024	TAT ACTTTTAATAATGTATAT TGTATTGTATCTGCATGATTTATTTAGAGTTCTTGTTTC	202083
QY	9781	ATCTTGTGTATATACTTAATTCGCTTTGT CATTTTGGAGACATTTATTTTGCCTCTCAATTT	9840
Db	202084	ATCTTGTGTATATACTTAATTCGCTTTGT CATTTTGGAGACATTTATTTTGCCTCTCAATTT	202143
QY	9841	CTTTACATTTTGTCTTACGGAATATTTTCA TTCACACTGTGGTAGCCGAATTAATCGTGT	9900
Db	202144	CTTTACATTTTGTCTTACGGAATATTTTCA TTCACACTGTGGTAGCCGAATTAATCGTGT	202203
QY	9901	TC TTCACCTTAGGACAT TGTCGTCTAAGTGTGAAGACAT TGCTTATTTTACCAGCAAC	9960
Db	202204	TC TTCACCTTAGGACAT TGTCGTCTAAGTGTGAAGACAT TGCTTATTTTACCAGCAAC	202263
QY	9961	CAT TC TGA AAGCATATGACAAAATTTTCTCTCTTAATCTTACTATATACTGAAAGCAGA	10020
Db	202264	CAT TC TGA AAGCATATGACAAAATTTTCTCTCTTAATCTTACTATATACTGAAAGCAGA	202323
QY	10021	CT GCTATAAGCCTTCAC TTACTCTTCTACCTCA TAAGGAATAT GTTTACAAATTAATTTAT	10080
Db	202324	CT GCTATAAGCCTTCAC TTACTCTTCTACCTCA TAAGGAATAT GTTTACAAATTAATTTAT	202383
QY	10081	AGGTPAACCA TTGTTTATAT TCGTTTTATTTCA CCTGGSGCTGAGATTTCAAGAACACC	10140
Db	202384	AGGTPAACCA TTGTTTATAT TCGTTTTATTTCA CCTGGSGCTGAGATTTCAAGAACACC	202443
QY	10141	CCAGCTCTTCAGGTAACACATTTTCACTTAACACATTTTACTAAACATCAGCAACTGTGGCCT	10200
Db	202444	CCAGCTCTTCAGGTAACACATTTTCACTTAACACATTTTACTAAACATCAGCAACTGTGGCCT	202503
QY	10201	GTTAAATTTTTTTTAA TAGAAATTTTAA GTCCTCATTTTCTTCGGTGTTTTTTAAAGCTTAA	10260
Db	202504	GTTAAATTTTTTTTAA TAGAAATTTTAA GTCCTCATTTTCTTCGGTGTTTTTTAAAGCTTAA	202563
QY	10261	TTTTTCTGGCTTTATTCATAAATCTTAAGGTCACACTACATTTTGAAAAATCAAAGACCTG	10320
Db	202564	TTTTTCTGGCTTTATTCATAAATCTTAAGGTCACACTACATTTTGAAAAATCAAAGACCTG	202623
QY	10321	CATTTTAAATTTCTTATTCACCTCTGCGAAAACCATTCACAAAACCATGGTAGTAAAGAGAA	10380
Db	202624	CATTTTAAATTTCTTATTCACCTCTGCGAAAACCATTCACAAAACCATGGTAGTAAAGAGAA	202683
QY	10381	GGGTGACACCTGTGGCCATAGGTAAATGTPACCA CGGTGCTCGGTTGACCAAGATGCAAG	10440

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Db	6345	TAGACACAAATAGGTGTCCTCCTGTAGTGTGTTTTTTCTGAAAGGGTATTTCCTTC	6404
Qy	5517	CTCCAACTATAGAAAGAGTGAAGTTCCAGTCTTCTCTGGCAAGGGTAAACAGATCCCC	5576
Db	6405	CTCCAACTATAGAAAGAGTGAAGTTCCAGTCTTCTGTGCAAGGGTAAACAGATCCCC	6464
Qy	5577	TCTCCTCATCCTTCCCTTTCTCTGTCAAGTGCTCTCTTTGGTGAAGGTGACACATCATGT	5636
Db	6465	TCTCCTCATCCTTCCCTTTCTCTGTCAAGTGCTCTCTTTGGTGAAGGTGACACATCATGT	6524
Qy	5637	GACCTCTTCAGTGACCACCTCTACGGTGTGCGGCCCTTGAACCTACTACCCCCAGAACATCAC	5696
Db	6525	GACCTCTTCAGTGACCACCTCTACGGTGTGCGGCCCTTGAACCTACTACCCCCAGAACATCAC	6584
Qy	5697	CATGAAGTGCTCAAGGATTAAGCAGCCAAATGATGCCAAGGAGTTCGAACCTAAAGACGT	5756
Db	6585	CATGAAGTGCTCAAGGATTAAGCAGCCAAATGATGCCAAGGAGTTCGAACCTAAAGACGT	6644
Qy	5757	ATTGCCCAATTGGGATTTGGACCTTACCAGGGCTGGAATAACCTTGGCTGTACCCCTGGGGA	5816
Db	6645	ATTGCCCAATTGGGATTTGGACCTTACCAGGGCTGGAATAACCTTGGCTGTACCCCTGGGGA	6704
Qy	5817	AGAGCAGAGATATACGTATCCAGGTGAGACACCAGGCCCTGGATCAGCCCCCTCATTTGTGAT	5876
Db	6705	AGAGCAGAGATATACGTATCCAGGTGAGACACCAGGCCCTGGATCAGCCCCCTCATTTGTGAT	6764
Qy	5877	CTGGGTTATGTGACTCATCAGAGCCAGGAGCTGAGAAATCTATTGGGGTTGAGAGGAG	5936
Db	6765	CTGGGTTATGTGACTCATCAGAGCCAGGAGCTGAGAAATCTATTGGGGTTGAGAGGAG	6824
Qy	5937	TGCCTGAGGAGTAAATATTGGCAGTGCATGAGGATCTGCTCTTTGTTAGGGGTGGGCT	5996
Db	6825	TGCCTGAGGAGTAAATATTGGCAGTGCATGAGGATCTGCTCTTTGTTAGGGGTGGGCT	6884
Qy	5997	GAGGTTGGCAATCAAGGCTTTAACTTGCTTTTCTGTTTTAGAGCCCTCACGCTCTGGC	6056
Db	6885	GAGGTTGGCAATCAAGGCTTTAACTTGCTTTTCTGTTTTAGAGCCCTCACGCTCTGGC	6944
Qy	6057	ACCTTAGTCATTGGAGTCATCAGTGGAAATGCTGTGTTTGTGCTCATCTTGTTCATTGGA	6116
Db	6945	ACCTTAGTCATTGGAGTCATCAGTGGAAATGCTGTGTTTGTGCTCATCTTGTTCATTGGA	7004
Qy	6117	ATTTTCTTCATTAATATTAGGAAGAGCCAGGGTTCAAGTGAGTAGGAACAAAGGGGGAAGT	6176
Db	7005	ATTTTCTTCATTAATATTAGGAAGAGCCAGGGTTCAAGTGAGTAGGAACAAAGGGGGAAGT	7064
Qy	6177	CTCTTAGTACTCTGCCCCAGGCCACAGTGGGAAGAGGGGCAGAGGGATCTGCGATCCA	6236
Db	7065	CTCTTAGTACTCTGCCCCAGGCCACAGTGGGAAGAGGGGCAGAGGGATCTGCGATCCA	7124
Qy	6237	TGGGAGGCAATTTTCTCATTTATATCTTTGGGACACCAGCAGCTCCCTGGGAGACAGA	6296
Db	7125	TGGGAGGCAATTTTCTCATTTATATCTTTGGGACACCAGCAGCTCCCTGGGAGACAGA	7184
Qy	6297	AAATAATGTTCTCTCCAGAAATGAAGTCTTAATTCACAACAACATCTTCAGAGCACCTA	6356
Db	7185	AAATAATGTTCTCTCCAGAAATGAAGTCTTAATTCACAACAACATCTTCAGAGCACCTA	7244
Qy	6357	CTATTTTGCAGAGCTGTTTAAAGTAGTACAGGGGCTTTGAGGTTGAGAAGTCACTGTGG	6416
Db	7245	CTATTTTGCAGAGCTGTTTAAAGTAGTACAGGGGCTTTGAGGTTGAGAAGTCACTGTGG	7304
Qy	6417	CTATTTCTGAACCCCAATCTGGTAGGAAATGAATTTGATAGCAGTAAATGTAGTTAAA	6476
Db	7305	CTATTTCTGAACCCCAATCTGGTAGGAAATGAATTTGATAGCAGTAAATGTAGTTAAA	7364
Qy	6477	GAAGACCCCATGAGTCTCTAAAGCAGGCAGGAACCAATGCTTAGGTTGCAAGGAAG	6536
Db	7365	GAAGACCCCATGAGTCTCTAAAGCAGGCAGGAACCAATGCTTAGGTTGCAAGGAAG	7424
Qy	6537	AATGATCACTACGCTGGGATCAAGATAGCCTTCTTGATCTTTGAAGGAGAAGCTGGAT	6596
Db	7425	AATGATCACTACGCTGGGATCAAGATAGCCTTCTTGATCTTTGAAGGAGAAGCTGGAT	7484

QY	6597	TCCATT	AGCTGAGGTTGAAGATGATGGAGGTCCTACACAGACGGAGCAACCATGCCAAGT	6695
Db	7485	TCCATT	TAGGTGAGGTTGAAGATGATGGAGGTCCTACACAGACGGAGCAACCATGCCAAGT	7544
QY	6657	AGGAGAT	TAAGGCATACCTGGGAGATTAGAAATAATTACTCTACCTTTAAACCCCTGAGTTT	6716
Db	7545	AGGAGAT	TAAGGCATACCTGGGAGATTAGAAATAATTACTCTACCTTTAAACCCCTGAGTTT	7604
QY	6717	GGTAGCT	TATCACTCAACAATTATGCAATTTCTACCCCTTGAAACATCTCTGGTGTAGGGAA	6776
Db	7605	GCTTAGCT	TATCACTCAACAATTATGCAATTTCTACCCCTTGAAACATCTCTGGTGTAGGGAA	7664
QY	6777	AAGGAAT	CAAAAGAACCCAGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTTGGGTT	6836
Db	7665	AAGGAAT	CAAAAGAACCCAGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTTGGGTT	7724
QY	6837	ATGATCA	CTGGGGTGTCTAATTGAAGGATCCTTAAGAAAGGAGGACCAACGATCTCCCTTATAT	6896
Db	7725	ATGATCA	CTGGGGTGTCTAATTGAAGGATCCTTAAGAAAGGAGGACCAACGATCTCCCTTATAT	7784
QY	6897	GGTGAAT	GTCTTTAGAAGTTTAGATGAGAGTGAGGAGACCAAGTTAGAAAGCCAATAA	6956
Db	7785	GGTGAAT	GTCTTTAGAAGTTTAGATGAGAGTGAGGAGACCAAGTTAGAAAGCCAATAA	7844
QY	6957	GCATTT	CCAGATGAGAGATTAATGGTTCTTTGAAATCCAATAGTGCCACGCTCTAAATTTGAG	7016
Db	7845	GCATTT	CCAGATGAGAGATTAATGGTTCTTTGAAATCCAATAGTGCCACGCTCTAAATTTGAG	7904
QY	7017	ATGGGT	GAATGAGGAAATTAAGGAAGAGAGAAGAGCAAGATGGTGCTAGGTTTGTGAT	7076
Db	7905	ATGGGT	GAATGAGGAAATTAAGGAAGAGAGAAGAGCAAGATGGTGCTAGGTTTGTGAT	7964
QY	7077	GCCTCT	TTTCTCGGTCTCTTGCTCTCCACAGGAGGAGCCATGGGCACTACGCTCTAGCTG	7136
Db	7965	GCCTCT	TTTCTCGGTCTCTTGCTCTCCACAGGAGGAGCCATGGGCACTACGCTCTAGCTG	8024
QY	7137	AACGTG	AGTGACGAGCCTCGAGACTCACTGTGGGAAGGAGACAAACCTAGAGACTCA	7196
Db	8025	AACGTG	AGTGACGAGCCTCGAGACTCACTGTGGGAAGGAGACAAACCTAGAGACTCA	8084
QY	7197	AAGAGG	AGATGCATTTATGAGCTTCATCTGTTCCAGGAGAGAGTTGAACCTTAACATAGA	7256
Db	8085	AAGAGG	AGATGCATTTATGAGCTTCATCTGTTCCAGGAGAGAGTTGAACCTTAACATAGA	8144
QY	7257	AATTGC	CTGACGAACCTCTTGATTTTAGCCTTCTCTGTTTCCATTTCCCAAAAAGATTCC	7316
Db	8145	AATTGC	CTGACGAACCTCTTGATTTTAGCCTTCTCTGTTTCCATTTCCCAAAAAGATTCC	8204
QY	7317	CCATTT	AGGTTTCTGAGTTCCCTGCATGCCGGTGATCCCTAGCTGTGACCTCTCCCTGGGA	7376
Db	8205	CCATTT	AGGTTTCTGAGTTCCCTGCATGCCGGTGATCCCTAGCTGTGACCTCTCCCTGGGA	8264
QY	7377	ACTGTC	CTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCCTCCGCTCACTC	7436
Db	8265	ACTGTC	CTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCCTCCGCTCACTC	8324
QY	7437	AGAGACA	TACACCTATGTCATTTTCCCTATTTTTGGGAAGGAGACTCCCTTAATTTGG	7496
Db	8325	AGAGACA	TACACCTATGTCATTTTCCCTATTTTTGGGAAGGAGACTCCCTTAATTTGG	8384
QY	7497	GGGACT	TTACATGATTCATTTTAAACATCTGAGAAAAGCTTTGAACCCCTGGGACCTGGCTAG	7556
Db	8385	GGGACT	TTACATGATTCATTTTAAACATCTGAGAAAAGCTTTGAACCCCTGGGACCTGGCTAG	8444
QY	7557	TCATPAC	CTTTACAGATTTTTACACATGTATCTATGCAATTTTCTGGACCCCGTTTCAACTTT	7616
Db	8445	TCATPAC	CTTTACAGATTTTTTACACATGTATCTATGCAATTTTCTGGACCCCGTTTCAACTTT	8504
QY	7617	TCCTTT	GAATCCCTCTCTGTGTTACCAGTAACATCATCTGTACCAAGCCTTTGGGGNTT	7676
Db	8505	TCCTTT	GAATCCCTCTCTGTGTTACCAGTAACATCATCTGTACCAAGCCTTTGGGGNTT	8564

QY 7677 CTTCCATCTGATTGTGATGTGACAGCTATGAAGCTGTACACTGCACGAATGGA 7736
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Db 8565 CTTCCATCTGATTGTGATGTGACAGCTATGAAGCTGTACACTGCACGAATGGA 8624
QY 7737 AGAGGCACCTGTCCCGAGAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGTGTGTTT 7796
Db 8625 AGAGGCACCTGTCCCGAGAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGTGTGTTT 8684
QY 7797 TAGCAGGTAGAGGCAAAATATCTTTGAAGGGTGTGAAGAGGTGTTTTTCTAAATGGC 7856
Db 8685 TAGCAGGTAGAGGCAAAATATCTTTGAAGGGTGTGAAGAGGTGTTTTTCTAAATGGC 8744
QY 7857 ATGAAGTGTCTATACAGATTGCAAAAGTTTAATGGTCCCTTCATTTGGGATGCTACTCTA 7916
Db 8745 ATGAAGTGTCTATACAGATTGCAAAAGTTTAATGGTCCCTTCATTTGGGATGCTACTCTA 8804
QY 7917 GTATTCAGACCTGAAGAACTACAAATTAATTTCTACCTGGTCTCTCTTGTCTGATAAT 7976
Db 8805 GTATTCAGACCTGAAGAACTACAAATTAATTTCTACCTGGTCTCTCTTGTCTGATAAT 8864
QY 7977 GAAAATTAATGAAGGATGATAAAGACATTACTTCGTGTCGACTCTCTGAGCACCTA 8036
Db 8865 GAAAATTAATGAAGGATGATAAAGACATTACTTCGTGTCGACTCTCTGAGCACCTA 8924
QY 8037 CTTACATGCATTACTGCATGCACCTCTCTTACAAATTAATTTCTATGAGATAGGTACTATTATCC 8096
Db 8925 CTTACATGCATTACTGCATGCACCTCTCTTACAAATTAATTTCTATGAGATAGGTACTATTATCC 8984
QY 8097 CCATTTCTTTTAAATGAAGAAAGTGAAGTGAAGCGGACGGTGGCTCACGCCCTGTAA 8156
Db 8985 CCATTTCTTTTAAATGAAGAAAGTGAAGTGAAGCGGACGGTGGCTCACGCCCTGTAA 9044
QY 8157 TCCAGCAGCTTTGGGAGGCCAAAGCGGTGGATCACGAGGTTCAGGAGATCGAGACCATCC 8216
Db 9045 TCCAGCAGCTTTGGGAGGCCAAAGCGGTGGATCACGAGGTTCAGGAGATCGAGACCATCC 9104
QY 8217 TGGCTAAACATGGTGAACCCCATCTCTTAATAAAAATACAAAAATTAAGCTGGGCGTGGT 8276
Db 9105 TGGCTAAACATGGTGAACCCCATCTCTTAATAAAAATACAAAAATTAAGCTGGGCGTGGT 9164
QY 8277 GCAGACGCTGTAGTCCAGCTACTTCGGAAGGCTGAGGCAGAGAAATGGATGAACCCAG 8336
Db 9165 GCAGACGCTGTAGTCCAGCTACTTCGGAAGGCTGAGGCAGAGAAATGGATGAACCCAG 9224
QY 8337 GAGCAGAGCTGTGAGTGAGCGGAGTTTGGCCACATGACATCCAGCCTVAGGTGACAGAGT 8396
Db 9225 GAGCAGAGCTGTGAGTGAGCGGAGTTTGGCCACATGACATCCAGCCTVAGGTGACAGAGT 9284
QY 8397 GAGACTCCATCTCAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAA 8456
Db 9285 GAGACTCCATCTCAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAA 9344
QY 8457 AGTATAGAGTATCTCATAGTTTGTGAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTG 8516
Db 9345 AGTATAGAGTATCTCATAGTTTGTGAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTG 9404
QY 8517 ACCGTTTGATACATCTGACACCACTACATTCAGTAGTTTAGATGCCATAGAAATAG 8576
Db 9405 ACCGTTTGATACATCTGACACCACTACATTCAGTAGTTTAGATGCCATAGAAATAG 9464
QY 8577 AGAAGGAAGGAGATGGCTCTCTCTGTCTCATTTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 8636
Db 9465 AGAAGGAAGGAGATGGCTCTCTCTGTCTCATTTGTCTCTCTCTCTCTCTCTCTCTCTCT 9524
QY 8637 ACATGAAGGGGAACAGCAGAAAACCACTGATCCCTCAGCTGTGATGTTTCCCTTTAAA 8696
Db 9525 ACATGAAGGGGAACAGCAGAAAACCACTGATCCCTCAGCTGTGATGTTTCCCTTTAAA 9584
QY 8697 AGTCCCTGAGGAAGGTCTGGAATGTGACTCCCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 8756
Db 9585 AGTCCCTGAGGAAGGTCTGGAATGTGACTCCCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 9644
QY 8757 TTCATTCTTTGGACCCCTACGCAAGGACTGTAAATGGTGGGACAGCTAGTGGCCCTGCT 8816
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Db 9645 TTCATTCTTTGGACCCCTACGCAAGGACTGTAAATGGTGGGACAGCTAGTGGCCCTGCT 9704
QY 8817 GGGCTTCACACACGGTGTCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTCTGTGTGTA 8876
Db 9705 GGGCTTCACACACGGTGTCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTCTGTGTGTA 9764
QY 8877 TTTCCCTCAATGAAGTGGAGTAAGCTCTCTCAATTTTGAGATGGTATAATGGAAGCACCA 8936
Db 9765 TTTCCCTCAATGAAGTGGAGTAAGCTCTCTCAATTTTGAGATGGTATAATGGAAGCACCA 9824
QY 8937 AGTGGCTTAGAGGATGCCAGGTCTCTCCATGGAGCCACTGGGGTTCGGGTGCGACATTAA 8996
Db 9825 AGTGGCTTAGAGGATGCCAGGTCTCTCCATGGAGCCACTGGGGTTCGGGTGCGACATTAA 9884
QY 8997 AAAAAAATCTAACGAGGACATTCAAGGAATTCAGATTCTCGGAAATCAGTTCACCATG 9056
Db 9885 AAAAAAATCTAACGAGGACATTCAAGGAATTCAGATTCTCGGAAATCAGTTCACCATG 9944
QY 9057 TTCAAAGAGTCTTTTTTTTTTTTTTTTGTAGACTCTATTTGCCAGGCTGGAGTGCATGGCA 9116
Db 9945 TTCAAAGAGTCTTTTTTTTTTTTTTTTGTAGACTCTATTTGCCAGGCTGGAGTGCATGGCA 10004
QY 9117 TGAATCTCGGCTCACTGTAACCTCTGCCTCCAGGTTCAAGCGATTCTCTCTGTCTCAGCT 9176
Db 10005 TGAATCTCGGCTCACTGTAACCTCTGCCTCCAGGTTCAAGCGATTCTCTCTGTCTCAGCT 10064
QY 9177 CCCAAGTAGCTGGGATTACAGGCTGCACACCATGCCCGCTAAATTTTGTATTTTGTAG 9236
Db 10065 CCCAAGTAGCTGGGATTACAGGCTGCACACCATGCCCGCTAAATTTTGTATTTTGTAG 10124
QY 9237 TAGAGACAGGGTTTACCATGTTGGCCAGGCTGGTCTGAACTCTCTGACCTCTGATC 9296
Db 10125 TAGAGACAGGGTTTACCATGTTGGCCAGGCTGGTCTGAACTCTCTGACCTCTGATC 10184
QY 9297 CGCTCGCTCGGCTCCCAAAGTGTGAGATTACAGGTGTGAGCCACCTGCCACCGCT 9356
Db 10185 CGCTCGCTCGGCTCCCAAAGTGTGAGATTACAGGTGTGAGCCACCTGCCACCGCT 10244
QY 9357 CAAAAGAGCTTTAAT 9416
Db 10245 CAAAAGAGCTTTAAT 10304
QY 9417 CTTGGCTGCATAAATCTGGTACAAAGCATCTGCTTTGAAGGCGAGGTCTTCAGGATACC 9476
Db 10305 CTTGGCTGCATAAATCTGGTACAAAGCATCTGCTTTGAAGGCGAGGTCTTCAGGATACC 10364
QY 9477 ATATACAGCTCAGAAGTTTCTCTTTTAGGCATTTAAATTTTAGCAAGATATCTCATCTCT 9536
Db 10365 ATATACAGCTCAGAAGTTTCTCTTTTAGGCATTTAAATTTTAGCAAGATATCTCATCTCT 10424
QY 9537 TCTTTTAAACCATTTCTTTTTTTTGTGGTTAGAAAAGTTTATGTAGAAAAAGTAAATGTG 9596
Db 10425 TCTTTTAAACCATTTCTTTTTTTTGTGGTTAGAAAAGTTTATGTAGAAAAAGTAAATGTG 10484
QY 9597 ATTTAGCTCATTTGTAGAAAAGCTATAAAATGAATACAATTAAGCTGTTATTTAATTAG 9656
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QY 9657 CCAGTGAAGAACTATTAAACAACTTGTCTATTTAGTGTATTTAGTGTGCAATTAATAA 9716
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QY 9717 TGCATATACATTTAATAAATGATATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 9776
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QY 9777 GTTCATCTTGTGATATACATTAATCGCTTTTGTCAATTTTGAGACATTTATTTTGTCTTA 9836
Db 10665 GTTCATCTTGTGATATACATTAATCGCTTTTGTCAATTTTGAGACATTTATTTTGTCTTA 10724
QY 9837 ATTTCTTTACATTTTGTCTTTACGGAATATTTTCATTCACCTGTGGTAGCGGATTAATCG 9896
|||||

Db	10725	ATTTCTTTACATTTTGTCTTAGGAAATATTTTCACTCAACTGTGTAGCCGAATTAATCG	10784
Qy	9897	TCGTTCTTCACTCTAGGACATTCGCTCAAGTGTGAAGACATGGTTATTTTACCAGC	9956
Db	10785	TGTTTCTTCACTCTAGGACATTCGCTCAAGTGTGAAGACATGGTTATTTTACCAGC	10844
Qy	9957	AAACCATCTCTGAAGCATATGACAAATATTTCTCTTATATCTTACTATATACTGAAAG	10016
Db	10845	AAACCATCTCTGAAGCATATGACAAATATTTCTCTTATATCTTACTATATACTGAAAG	10904
Qy	10017	CAGACTGCTATAAGGCTTCACTTACTCTTACCTCATATAGGAATATGTTCACAAATTAAT	10076
Db	10905	CAGACTGCTATAAGGCTTCACTTACTCTTACCTCATATAGGAATATGTTCACAAATTAAT	10964
Qy	10077	TATTAGGTAAGCATTTGTTTATATATGTTTATTTTACCTGGCTGAGATTTCAAGAA	10136
Db	10965	TATTAGGTAAGCATTTGTTTATATATGTTTATTTTACCTGGCTGAGATTTTCAAGAA	11024
Qy	10137	CACCCAGCTTCTACAGTAACACATTTTCACTTAACACATTTTACTAAACATCAGCAACTGTG	10196
Db	11025	CACCCAGCTTCTACAGTAACACATTTTCACTTAACACATTTTACTAAACATCAGCAACTGTG	11084
Qy	10197	GCCTGTTAAATTTTAAATAGAAATTTTAACTCCTCAATTTTTCGGTGTGTTTTTAAGC	10256
Db	11085	GCCTGTTAAATTTTAAATAGAAATTTTAACTCCTCAATTTTTCGGTGTGTTTTTAAGC	11144
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Db	11145	TAAATTTTCTGCTTATTTATATATATTTTAAAGTCAACTACATTTTGAAGAAATCAAGA	11204
Qy	10317	CCTGCATTTTAAATCTTATTTACCTCTGGCAAAACCATTTCAAAACCATGGTAGTAAAG	10376
Db	11205	CCTGCATTTTAAATCTTATTTACCTCTGGCAAAACCATTTCAAAACCATGGTAGTAAAG	11264
Qy	10377	AGAGGTGACACCTGGTGGCCATAGTAAATGACACCGTGGTTCGGGTGACACAGAT	10436
Db	11265	AGAGGTGACACCTGGTGGCCATAGTAAATGACACCGTGGTTCGGGTGACACAGAT	11324
Qy	10437	GCAGCGTGGAGGTTTTCCTCAAGGTAAGGAATAAGATGATGGTGGAGGGCGTGCAC	10496
Db	11325	GCAGCGTGGAGGTTTTCCTCAAGGTAAGGAATAAGATGATGGTGGAGGGCGTGCAC	11384
Qy	10497	GGAAATCACTTGTAGAGAAAGCCCTGAAATTTGAGAAAACAAACAAAGAACTACTTA	10556
Db	11385	GGAAATCACTTGTAGAGAAAGCCCTGAAATTTGAGAAAACAAACAAAGAACTACTTA	11444
Qy	10557	CCAGCTATTTCAATTTGCTGGAATCAGAGCCCATTTGCTGACCTGCTGAACCTGGGAACA	10616
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Db	11505	ACAGAAGAAACAAACCACTCTGATAATCATTTGAGTCAAGTACAGCGTGAATTCAGGA	11564
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Db	11565	CTGCTGAGAGGTACAGGCCAAAATTTCTATGTTATTAATAATGTCATCTTATAATA	11624
Qy	10737	CTGTCATATTTTATAAAACATTTCTCACAACCTCACACATTTTAAAAACAAACACTG	10796
Db	11625	CTGTCATATTTTATAAAACATTTCTCACAACCTCACACATTTTAAAAACAAACACTG	11684
Qy	10797	TCCTTAAATCCCAATTTTTCATAAAC	10825
Db	11685	TCCTTAAATCCCAATTTTTCATAAAC	11713

RESULT 5
AL359892/c
LOCUS
DEFINITION Homo sapiens chromosome 6 clone RP11-557F22, *** SEQUENCING IN
PROGRESS ***, 18 unordered pieces.
ACCESSION AL359892

VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AL359892.5 GI:9930971
HTG; HTGS_PHASE1.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 193752)
Sims, S.
Direct Submission
Submitted (19-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Aug 27, 2000 this sequence version replaced gi:9864230.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA557F22
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 183925 bases at least Q40
Consensus quality: 187703 bases at least Q30
Consensus quality: 189658 bases at least Q20
Insert size: 192052; sum-of-contigs
Insert size: 198247; agarose-fp
Quality coverage: 3.68x in Q20 bases; sum-of-contigs Quality
coverage: 3.70x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 3250: contig of 3250 bp in length
* 3251 3350: gap of 100 bp
* 3351 14600: contig of 11250 bp in length
* 14601 14700: gap of 100 bp
* 14701 32357: contig of 17657 bp in length
* 32358 32457: gap of 100 bp
* 32458 34886: contig of 2429 bp in length
* 34887 34986: gap of 100 bp
* 34987 43490: contig of 8504 bp in length
* 43491 43590: gap of 100 bp
* 43591 47437: contig of 3847 bp in length
* 47438 47537: gap of 100 bp
* 47538 57356: contig of 9819 bp in length
* 57357 57456: gap of 100 bp
* 57457 59845: contig of 2389 bp in length
* 59846 59945: gap of 100 bp
* 59946 63972: contig of 4027 bp in length
* 63973 64072: gap of 100 bp
* 64073 82711: contig of 18639 bp in length
* 82712 82811: gap of 100 bp
* 82812 111814: contig of 29003 bp in length
* 111815 111914: gap of 100 bp
* 111915 120276: contig of 8362 bp in length
* 120277 120376: gap of 100 bp
* 120377 136660: contig of 16284 bp in length
* 136661 136760: gap of 100 bp
* 136761 153913: contig of 17153 bp in length
* 153914 154013: gap of 100 bp
* 154014 158659: contig of 4646 bp in length
* 158660 158759: gap of 100 bp
* 158760 164235: contig of 5476 bp in length
* 164236 164335: gap of 100 bp
* 164336 184996: contig of 20661 bp in length

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QY 2041 ----- 2040
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QY 2041 -----CGGCGTGGGGGTGGGAAGGGGGGACTACCATCTGCA 2075
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Db 13980 TTCTCTACAAAATAACAAAATTTAGCTGGGTGTGGTCATGCACCTGTGATCCTAGCT 13921
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Db 13860 CATGACTGTGCCACTGTACTTTCAGCTTAGGTGACAGAGCAAGACCCTGTCCCTCGACC 13801
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Db 13561 GGCTCACTTCTGTAATCCAGCACTTTGGTGGCTGAGGCAGGTAGATCATTTTTCAGGTTCAG 13502
QY 3156 GAGTTTGAGACAAAGCTTTGGCCAACTGGTGAACCCCATCTCTACTAAAAATACAAAAT 3215
Db 13501 GAGTTTGAGACAAAGCTTTGGCCAACTGGTGAACCCCATCTCTACTAAAAATACAAAAT 13442
QY 3216 TAGCCTGGTGTGGGGCAGCCCTATAGTCCAGGCTTTTCAGGAGGCTTAGGTAGGAGA 3275
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Db 13381 ATCCCTTGAACCCAGGAGGTGCAGTTTGCAGTGAGCTGAGATTGTGCACCTGCACCTCCAG 13322
QY 3336 CCTGGGTGATAGGTGAGACTGTCTCTC-----AAAAAAAAAAAAAAAAAAAAAAAAA 3390

Db 13321 CCTGGGTATAGATGAGACTCTGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAA 13262
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Db 13081 GTGGCAGAGAAAAACACACAGGAAAGACAGCACCGAGACTGTCATATGGAAGAAAGACAG 13022
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Db 13021 GACTGCAACTCACCCTTACAAAATGAGGACACAGACAGCTGATGATGATGATGATGATG 12962
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Db 12901 TCTGTCTCCAGGTTACACACTCTCTGCACTACCTTCTCATGGTGCCTCAGAGCAGGACCT 12842
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Db 12601 CCTGAGGTTGTGAGAGCTTTTCACTTTTTCATGCTCTTGAAGGAAACAGCTGGAAGTCT 12542
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Db 12541 GAGTCTTTGTGGAGCAGGAGGAAAGGAAATTTGCTTCTGAGATCATTTGGTCTCTT 12482
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Db 12481 GGGATGGTGGAAATAGGACCTATTCTTTGTTGCTGAGTTACAGAGCTGGGGATTTT 12422
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Db 12421 CCAGAGTCCACACCCCTGCAAGTCTCCTGGGCTGTGAATGCAAGAACACAGTACC 12362
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Db 12361 GAGGGCTACTGGAAGTACGGGTATGATGGGACGACCACTTGAATTTCTGCCCTGACACA 12302
Qy CTGGATTTGGAGACAGACAGACCCAGGGCTGCCACACAGCTGGAGTGGGAAAGGCAC 4410
Db 12301 CTGGATTTGGAGACAGACAGACCCAGGGCTGCCACACAGCTGGAGTGGGAAAGGCAC 12242
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Db 12181 CAGTTGCTGAGACTGGGAGAGGTGTTTTGGACCAACAGGTATGTTGGAAACACACTTC 12122
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RESULT 6
HSU91328/c
LOCUS
DEFINITION
Human hereditary haemochromatosis region, histone 2A-like protein
gene, hereditary haemochromatosis (H2A-H) gene, Ror1 gene, and
sodium phosphate transporter (NPT3) gene, complete cds.
ACCESSION
U91328
VERSION
U91328.1
GI:2088550
KEYWORDS
human.
SOURCE
Homo sapiens
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 246282)
AUTHORS
Ruddy D.A., Krommal, G.S., Lee, V.K., Mintier, G.A., Quintana, L.,
Domingo, R., Jr., Meyer, N.C., Irrinke, A., McClelland, E., Fullan, A.,
Mapa, F.A., Moore, T., Thomas, W., Loeb, D.B., Harmon, C.,
Tsuchihashi, Z., Wolff, R.K., Schatzman, R.C. and Feder, J.N.
A 1.1 megabase transcript map of the hereditary hemochromatosis
locus
JOURNAL
Unpublished
REFERENCE
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AUTHORS
Ruddy D.A., Krommal, G.S., Lee, V.K., Mintier, G.A., Quintana, L.,
Domingo, R., Jr., Meyer, N.C., Irrinke, A., McClelland, E., Fullan, A.,
Mapa, F.A., Moore, T., Thomas, W., Loeb, D.B., Harmon, C.,
Tsuchihashi, Z., Wolff, R.K., Schatzman, R.C. and Feder, J.N.
Direct Submission
JOURNAL
Submitted (26-FEB-1997) Sequencing, Mercator Genetics, 4040
Campbell Avenue, Menlo Park, CA 94025, USA
FEATURES
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RESULT 7

AL353759
LOCUS
DEFINITION

AL353759 101099 bp DNA PRI 20-OCT-2000
Human DNA sequence from clone RPI-221C16 on chromosome 6. Contains STSs, GSSs, ESTs and CpG islands. Contains the 3' part of the HFE gene for haemochromatosis protein with two isoforms, two genes for novel histone 4 family members, two genes for novel histone 1 family members, three genes for novel histone 2B family members, a gene for a novel histone 2A family member and a novel pseudogene, complete sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 101099)

Williams, S.

Direct Submission

Submitted (20-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

request: clonerequest@sanger.ac.uk

On Jun 26, 2000 this sequence version replaced gi:8655345.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

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ACCESSION Y09799
VERSION Y09799.1 GI:2370109
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1479)
AUTHORS Carella and Gasparini,P.
TITLE Hereditary hemochromatosis genomic structure and organization of
HLA-H gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1479)
AUTHORS Gasparini,P.
TITLE Direct Submission
JOURNAL Submitted (04-DEC-1996) P. Gasparini, Servizio de Genetica Medica -
IRCCS, "Ospedale CSS", Via Cappuccini, 71013 S Giovanni, Rotondo
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DEFINITION AF301592
ACCESSION AF301592
VERSION AF301592.1 GI:11692702
KEYWORDS
SOURCE black rhinoceros.
ORGANISM Diceros bicornis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 4349)
West.C.J., Worley,M. and Beutler,E.
Rhinoceros HFE Polymorphisms
Unpublished
2 (bases 1 to 4349)
West.C.J., Worley,M. and Beutler,E.
Direct Submission
Submitted (30-AUG-2000) Molecular and Experimental Medicine, The
Shrapps Research Institute, 10550 North Torrey Pines Road, La
Jolla, CA 92037, USA
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QY 3882 GCCGTGTGGAGCCCGCAACTCCATGGGTTTCCAGTGAATAATTTCAAGCCAGATGGGTCG 3941
Db 121 GCCGTGCAGAGTCCCGTGCCTAGTGGGTCTTGGGTGAGGCCACAGCCAGCTGTGGCTGC 180
QY 3942 AGCTGAGTCAGAGTCTGAAAGGTTGGGATCACATGTTCACTGTTGACATCTCGGACTATTA 4001
Db 181 AACTGACTCAGAGCTGAAAGGTTGGGATCACATGTTCACTGCTGACTCTCGGACCATCA 240
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Db 301 TGGAGTGTTCCTTACCTCAAGGATGCATCTTGAAGGAGAGAGCTGAGAGTTTGAAGTCC 360
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QY 4238 CCCACACCTCGCAGGTCATCTTGGGCTGTAATCAAGAACACACAGTACCGAGGCT 4297
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QY 4298 ACTGGAAGTACGGGTATGATGGCAGGACCTTGAATTTCTCCCTGACACACTGGATT 4357
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Query Match	9.7%	Score 1051.6	DB 97	Length 2727
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QY 1225	CAAGAGGCGCCATGGGCACTACGCTT	TAGCTGAACCTGAGTCGACGCGAGCCTGCAGAC	1284	
DB				
QY 7164	TCACCTGTGGGAAGGAGACAAACCT	TAGAGACTCAAAGAGGAGTGCAATTTATGAGCTCTTC	7223	
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QY 1285	TCACCTGTGGGAAGGAGACAAACCT	TAGAGACTCAAAGAGGAGTGCAATTTATGAGCTCTTC	1344	
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QY 7224	ATGTTTCAGGAGAGAGTTGAACCTT	AAACATAGAATTCCTGACGAACTCCCTGATTTA	7283	
DB				
QY 1345	ATGTTTCAGGAGAGAGTTGAACCTT	AAACATAGAATTCCTGACGAACTCCCTGATTTA	1404	
DB				
QY 7284	GCCTTCTCTGTTCAATTTCTCTCAA	AAAGATTTCGCCATTTAGGTTCTGAGTTCCTGCATG	7343	
DB				
QY 1405	GCCTTCTCTGTTCAATTTCTCTCAA	AAAGATTTCGCCATTTAGGTTCTGAGTTCCTGCATG	1464	
DB				
QY 7344	CCGGTGATCCCTAGCTGTGACCTCT	CCCTCGGAACCTGCTCTCATGAACCTCAAGCTGCA	7403	
DB				
QY 1465	CCGGTGATCCCTAGCTGTGACCTCT	CCCTCGGAACCTGCTCTCATGAACCTCAAGCTGCA	1524	
DB				
QY 7404	TCTAGAGGCTTCCTTCATTTTCTCG	TGTCACCTCAGAGACATACACCTATGCTATTTCAAT	7463	
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QY 7464	TCCTATTTTGAAGAGAGACTCCCTT	AAATTTGGGGACTTACATGATTTTAACTC	7523	
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QY 7524	TGAGAAAAGCTTTGAACCTTGGAC	GTGGCTAGTCATAAGCTTACCAGATTTTACACAT	7583	
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QY 1645	TGAGAAAAGCTTTGAACCTTGGAC	GTGGCTAGTCATAAGCTTACCAGATTTTACACAT	1704	
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QY 7584	GTATCTATCCATTTCTCGACCCGTT	CAACTTTCCCTTGAATCTCTCTGTGTAC	7643	
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QY 1705	GTATCTATCCATTTCTCGACCCGTT	CAACTTTCCCTTGAATCTCTCTGTGTAC	1764	
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QY 7644	CAGTAACCTATCTGCACCAAGCCTT	GGGATCTTCCATCTGATTTGATGTGAGTTGC	7703	
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QY 1765	CAGTAACCTATCTGCACCAAGCCTT	GGGATCTTCCATCTGATTTGATGTGAGTTGC	1824	
DB				
QY 7704	ACAGCTATGAAGGCTGTACACTGC	ACGAATGGAAAGGACCTGTCCCGAAGAAAGCATC	7763	
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QY 1825	ACAGCTATGAAGGCTGTACACTGC	ACGAATGGAAAGGACCTGTCCCGAAGAAAGCATC	1884	
DB				
QY 7764	ATGGCTATCTGTGGGTAGTATGAT	GGGTGTTTTTACGAGGTAGAGGCAAAATCTTGAA	7823	
DB				
QY 1885	ATGGCTATCTGTGGGTAGTATGAT	GGGTGTTTTTACGAGGTAGAGGCAAAATCTTGAA	1944	
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QY 7884	TTTAATGGTGCCTTCATTTGGATG	CTACTAGTATTTCCAGACCTGAAAGATCAATA	7943	
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QY 2005	TTTAATGGTGCCTTCATTTGGATG	CTACTAGTATTTCCAGACCTGAAAGATCAATA	2064	
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QY 7944	ATTTTCTACCTGGTCTCTCTTGTTC	GTATGAATAAGAAATTTATGATGAAGATGATAAAGC	8003	
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QY 8004	ACTTACTTCGTCGCACTCTCTGAG	CACCTACTTACATGCATTAATGATGCACCTCT	8063	
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QY 2125	ACTTACTTCGTCGCACTCTCTGAG	CACCTACTTACATGCATTAATGATGCACCTCT	2184	
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QY 8064	TACAATAATTTCTAGATAGGTACT	ATATFCCCATTTCTTTTAAATGAAGAAGTG	8123	
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DEFINITION	Homo sapiens hemochromatosis splice variant delE3 mRNA, complete cds.		
ACCESSION	AF144242		
VERSION	AF144242.1	GI:11094324	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1885)		
TITLE	Thénie,A., Orhant,M., Gicquel,I. and Mosser,J.		
JOURNAL	HFE alternate splice variants		
REFERENCE	2 (bases 1 to 1885)		
AUTHORS	Thénie,A., Orhant,M., Gicquel,I. and Mosser,J.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-APR-1999) Faculte de Medecine, UPRA1 CNRS, 2 Avenue du Pr. Leon Bernard, Rennes Cedex 35043, France		
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Qy	7164	TCACTGTGGGAAGGAGACAAAACCTAGAGACTCAAGAGGGAGTGCATTATGAGCTCTTC	7223
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Qy	7224	ATGTTTCAGGAGAGATTGAACCTAAACATAGAAATTCCTGACGAACCTCCTTGATTTTA	7283
Db	971	ATGTTTCAGGAGAGATTGAACCTAAACATAGAAATTCCTGACGAACCTCCTTGATTTTA	1030
Qy	7284	GCCTCTCTGTTTCATTTTCCTCAAAAAGATTTCCTCCCATTTAGGTTTCTGAGTTCCTGCATG	7343
Db	1031	GCCTTCTCTGTTTCATTTTCCTCAAAAAGATTTCCTCCCATTTAGGTTTCTGAGTTCCTGCATG	1090
Qy	7344	CCGTGTATCCCTAGCTGTGACCTCTCCCTCGAACTGTCTCTCATGAACCTCAAGCTGCA	7403

Db 1091 CCGGTATCCCTAGCTGTGACCTCTCCCTGGAACTGTCTCTCATGAACCTCAAGCTGCA 1150
Qy 7404 TCTAGAGGCTTCCTTCAATTCCTCCGTCACCTCAGAGACATACACCTATGTCATTTTCATT 7463
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LOCUS H.sapiens HFE gene, exon 2 & 3.
DEFINITION H.sapiens HFE gene, exon 2 & 3.
ACCESSION Y09800
VERSION Y09800.1 GI:2370112
KEYWORDS HFE gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 874)
AUTHORS Carella and Gasparini, P.
TITLE Hereditary hemochromatosis genomic structure and organization of
HLA-H gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 874)
AUTHORS Gasparini, P.

TITLE Direct Submission
JOURNAL Submitted (04-DEC-1996) P. Gasparini, Servizio de Genetica Medica -
IRCCS, 'Ospedale CSS', Via Cappuccini, 71013 s Giovanni, Rotondo
(FG), ITALY
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Best Local Similarity 99.4%; Pred. No. 1.7e-173;
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Qy 4031 TGGAGAGGGGCTCACCTTCTGAGTTGTCAGAGCTTTTTCATCTTTTCATGATCTTG 4090
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RESULT 13
AF184234
LOCUS
DEFINITION Homo sapiens hereditary haemochromatosis protein precursor (HFE)
gene, partial cds.
ACCESSION AF184234
VERSION AF184234.1 GI:6010710
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 772)
AUTHORS Kutlar,F., Stomek,E., Holley,L., Leithner,C., Nechtman,J. and
Kutlar,A.
TITLE Two different mutations found in intron 4 of the human
hemochromatosis gene, in a Turkish family
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 772)
AUTHORS Kutlar,F., Stomek,E., Holley,L., Leithner,C., Nechtman,J. and
Kutlar,A.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-1999) Medicine/Hematology/Oncology/Sickle Cell
Center, Medical College of Georgia, 15 th St., AC-1000, Augusta, GA
30912, USA

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Query Match 7.13; Score 768.8; DB 89; Length 772;
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Db 181 TACGGTCTGGGGCTTGAACCTACTACCCCAAGACATCACCATCAAGTGCCTGAAGATA 240
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RESULT 14
AF301591
LOCUS
DEFINITION Ceratotherium simum HFE gene, exon 1 and partial cds.
ACCESSION AF301591

VERSION	AF301591.1	GI:11692700	
KEYWORDS	white rhinoceros.		
SOURCE	Ceratotherium simum		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.		
REFERENCE	1 (bases 1 to 3334)		
AUTHORS	West,C.J., Worley,M. and Beutler,E.		
TITLE	Rhinoceros HFE Polymorphisms		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 3334)		
AUTHORS	West,C.J., Worley,M. and Beutler,E.		
TITLE	Direct Submission		
JOURNAL	Submitted (30-AUG-2000) Molecular and Experimental Medicine, The Scripps Research Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA		
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Best Local Similarity 66.7%; Pred. No. 3.9e-153;			
Matches 1638; Conservative 0; Mismatches 653; Indels 166; Gaps 34;			
QY	234	GGAAGTTTACTGGGCATCTCTGAGCCTAGGCAATAGCTGTAGGGTGACTTTGGAGCC	293
DB	17	GAAGTTTTTCTGAGATTCCCGGAGCTCGGCAATGCTGCGAGGTGACTTCTTGGGTC	76
QY	294	ATCCCGCTTCCCGCCGCCCAAGAGCGGAGATTACGGGGAGCTGCGCCAGAGC	353
DB	77	ACTCCTATTTCGCGCCGCCACGAGCAGCTGACA-CGGGCCAGACCCGCGTCCGAGC	135
QY	354	TGGGAAATGGCCGCGGAGCGCGGCTTCTCTCTGATGCTTTTGAGACCCG	413
DB	136	CGGGAAATGGCCGCGGAGCGCCGACCCGCGCTTCTCTCTGATGCTTCTCTGCGGACCGT	195
QY	414	GTCTCTGAGGGCGCTTGTGCTGAGTCGAGGGCTGCGGGGAACTAGGGCGCGGC	473
DB	196	GCGCGGAGGGGCGGACCGCTGAGTCTGCGGGCTGCGGGCAAGACAGAGGGCGCGC	255
QY	474	GGGGTGGAAATCGAACTAGCTTTTCTGCGCTTGGAGTTTGTAACTTTGGAG	533
DB	256	GGGGGAGGAAATCGAAACGAGC-TTTCTAGCGCTTGGAGTTTGTAACTTTGGAG	314
QY	534	GACCTGCTCAACCTTATCCGCAAGCCCTCTCTCTGATTTCTGCGGTCAGACCCCGT	593
DB	315	GAACCTCTCAGCCCGCTGCGGAGTCCCTCCCGCAACTTTCCCGGGGGTGTCTCC--GGG	372
QY	594	GGAGTGCTTACACTGAAGTGCAGATAGGGGTCTCGCCCGAGGACCTGCCCTCCCG	653
DB	373	CAGTGGATGCACATCGGGTATGGGGCTCTCGCGGCAAGACCCCTGTCTCCCTCCCGC	432
QY	654	CGGCTGCTCCGCGCTCTGGGAGTGACTTTTGGAAACCGCCCACTCCCT-TCCCGCAACTAG	712
DB	433	CCCTGTCTCTCTCTCTCAGAGGACACTCGGAACCACTACTTCTCTCTCCCGGATCGT	492
QY	713	AATGCTTTTAAATAATCTCGTAGTTCCTCACTTGAAGCTAGAGCTTGGGGCTCTT	772
DB	493	GACTCTTTTAAATAATAATCTCTCGTTCTCTCACTAGGCGGAGCTAGGCTTGGGGACCTTG	552
QY	773	GAACTTGGAACTCGGGTT-TAFTTCCAATGTACGTGTGACAGTTTTCCTCCCACTCATCT	831
DB	553	GACTCAGATCTTGGTTTCTTCTCTCTGATTTTGTGTTTATCCCTGCTCATCC	612
QY	832	CMAACAGAAAGTTTCTTCC	851
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QY	852	-----TGAGTGTCTGCCGAGAAAGGCTGGGAGGCATTTGGCTGAGTGAACCCGCGCGGATC	893
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QY	954	TTGGGATCTGAATTTCTTCAACCATTTCCACCCACTTTTGGTGAGACCTGGGTGGAGGTC	1013
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QY	1014	CT-AGGCTGGGAGGCTCTGAGAGAGGCTTACCTCGGGCTTTCCCACTCTTTGGCAATT	1072
DB	853	CTGGGGTGGAGGCTCTGAGAGATATCTGCCCTGGGCT-CACGGACTCTCGGCGATT	911
QY	1073	GTCTTTTGGCTGGAAATTA--AGTATATGTTAGTTTGAACGTTTGAACGTTTGAACGTTTGA	1125
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DB	1032	AGGCTTTTACTAAAGGATGCCAAGTGGTGAATTAACATTAAGTGAAGTGAAGTGAAGTGAAGT	1091
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QY	1348	GTTTACAAAGAACATAAATAATCTGTTTCTGATTTTCACTAGGCATAGGAGTGTCT	1407
DB	1210	GGTTACAAAGAAATTTAGGCAATCGGTTTCTGATGTTTAAATGAAGTACTACACCTGCT	1269
QY	1408	CTAATCTTAGTTGACAGTGATTTTGCCTCTGATGTAGCACAGTGTCTGTG--GGTACA	1466
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DB	1390	ACAAGAATAAGCAT-----GACTTGTCTACTGTAACATTTATTTGTTTACTCTGTGC	1444
QY	1587	TTTGTGTCAGAGCTCATGTCTCCACTTCATAGTATGATTTTAAACATCACACTGCAT	1646
DB	1445	TTGTGAGGCAAAACCCATGTCTCCACTTCGTAAGTGGGATTCACACATTCACATTCAT	1504
QY	1647	TAGAGTTTGAATAATAAATTTTCACTGTGACAGAAATTTTCAATGTTTACAAGTGA--	1705
DB	1505	CAGAGTTTGAATCATACATTTGATTTTGAACAAAGATTTTCAATGTTTCAAGTGTACC	1564
QY	1706	ATGACTTCCAGCCATGTGTTGCTGCTTCAAGCCCGGAGGAGAGAGGAGGAGGAGGAGG	1765
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QY	1766	CTTTACCCCTTTGATATTTTGCATTTCTAGTGGGAGAGATGACAATAAGCAAAATGAGCAGAA	1825
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QY	1826	AGATATACAACATCATCAGAAATCATGGGTGTGTGAGAAAGCAGA-----GAAGTCAGGSCA	1880
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Db	1741	GGCCCTTTTCTCAGGCTGGTGCAGCAGTGACCTGAAGGAACAAAGAGTGATGCTTAAT	1800
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Db	1801	TGGGAGCAGCAGCTT--CCTGGCAAACTGGGTGTGCTGGCAGATTGGGTGTGAAGCAGGGTT	1859
QY	1999	TTTCTCAGCACTACTCTGCTGTGTGTGTGGGGGGGGGGGGCGCGGTGGGGGTGGGAAG	2058
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Db	1895	GGGAGCTGTCATGTGCACCTGCAGGATGTTTAGCAGCAT-CTTTGTCTTTTACTCTCTGGA	1953
QY	2118	TGCTAGGAGCACTCCCCAGTCTTTGACACCAAAAATGTCTCTAAACCTTTGCCACATGTC	2177
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QY	2236	CTG-----GGGAGTAGAGGCCAAGAAGTAGTAGTAATGGGCTCAGAGAGGAGC	2282
Db	2073	GTGTAGCACAGTAGTCAGGGAGGAGGGGTCAAGAAATT--GGTGGTGGGCTCAGTAAAGAGT	2131
QY	2283	CACAAACAGGTTGTGAGGGCGCTGTAGGCTGTGAGTGTGAATTTCTAGCCCAAGGAGTAAC	2342
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QY	2343	AGTGATCTGTCACAGGCTTTTAAAGATTGCTCTGGCTGTATGTGTGAAAGCAGCAATGAA	2402
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QY	2403	GGGAGCACACTAAAGCAGGAGCCAGCCAGGAACTGTTTACAC-AGTCCAGGCAAGA	2461
Db	2244	GGGAGCAACAATTAAAGCAGGGAGAGCAGCCAGGAAGCTGTGTGCACTAATCCAGGCAAGA	2303
QY	2462	GGTAGTGGAGTGGGCTGGGTGGGAACAGAAAAGGAGGTGACAAACCAATTCCTCTCTGAAT	2521
Db	2304	GATGATGCAATTGGGCCCTGGTTGGAGCAGAGGTGGTGGTGAAGAACCGTTGATTTTGGAT	2363
QY	2522	ATATTCTGAAGGAAGTTGCTGAAGGAT-TCTATGTTGTGTGAGAGAAAGAGAAGAT	2577
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DEFINITION	Homo sapiens hemochromatosis splice variant 620-1530del mRNA, complete cds.		
ACCESSION	AF144238		
VERSION	AF144238.1		
KEYWORDS	GI:11094316		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 794)		
TITLE	Thenie,A., Orhant,M., Gicquel,I. and Mosser,J.		
JOURNAL	HFE alternate splice variants		
	Unpublished		

REFERENCE	2 (bases 1 to 794)			
AUTHORS	Thenie,A., Orhant,M., Gicquel,I. and Mosser,J.			
TITLE	Direct Submission			
JOURNAL	Submitted (20-APR-1999) Faculte de Medecine, UPR41 CNRS, 2 Avenue du Pr. Leon Bernard, Rennes Cedex 35043, France			
FEATURES	Location/Qualifiers			
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	Query Match			
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	Matches 723; Conservative 0; Mismatches 2; Indels 4; Gaps 4;			
QY	7409	AGGCTTCCTTCATTTCCCTCCGACCTCAGACATACACCTATGTCATTTTCATTTCCCTA	7468	
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QY	7469	TTTTTGAAGAGGACCTTAAATTTGGGGACTTACATGATTCATTTTAAATCTGAGA	7528	
Db	130	TTTTTGAAGAGGACCTTAAATTTGGGGACTTACATGATTCATTTTAAATCTGAGA	189	
QY	7529	AAAGCTTTTGAACCCCTGGGACCTGGGTAGTCATAACCTTACCAGATTTTACACATGTATC	7588	
Db	190	AAAGCTTTTGAACCCCTGGGACCTGGGTAGTCATAACCTTACCAGATTTTACACATGTATC	249	
QY	7589	TATGCAATTTTCGGACCCCTTCACTTTTCCCTTTGAATCCTCTCTGTGTTTACCAGTA	7648	
Db	250	TATGCAATTTTCGGACCCCTTCACTTTTCCCTTTGAATCCTCTCTGTGTTTACCAGTA	309	
QY	7649	ACTCATCTCTCACCAGCCCTTGGGATTCCTCCATCTGATGTCAGTTGACAGC	7708	
Db	310	ACTCATCTCTCACCAGCCCTTGGGATTCCTCCATCTGATGTCAGTTGACAGC	368	
QY	7709	TATGAAGGCTGTACACTGCACGAATGGAAGAGGCACCTGTCCAGAAAAGCATCATGGC	7768	
Db	369	TATGAAGGCTGTACACTGCACG-ATGGAAGAGGCACCTGTCCAGAAAAGCATCATGGC	427	
QY	7769	TATCTGTGGGTAGTATGATGGGTGTTTTTAGCAGGTAGGAGCAATATCTTTGAAGGGG	7828	
Db	428	TA-CTGTGGGTAGTATGATGGGTG-TTTTAGCAGGTAGGAGCAATATCTTTGAAGGGG	485	
QY	7829	TTGTGAAGAGGTGTTTTTTTCTAATTGGCATGAAGGTGTCATACAGATTTGCAAGCTTAA	7888	
Db	486	TTGTGAAGAGGTGTTTTTTCTAATTGGCATGAAGGTGTCATACAGATTTGCAAGCTTAA	545	
QY	7889	TGGTGCTTCATTTGGGATGCTACTCTAGTATTCAGACCTTGAAGAATCACAATAATTTT	7948	
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 6, 2001, 08:29:41 ; Search time 584.14 Seconds
(without alignments)
11635.969 Million cell updates/sec

Title: US-09-497-957-3

Perfect score: 10825

Sequence: 1 TCTAAGTTGAGATAAAATT.....TCCCAAAATTTTCATAAAC 10825

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10825	100.0	10825	22 AAC68426	Human hereditary h
2	10823.4	100.0	10825	22 AAC68425	Human hereditary h
3	10823.4	100.0	10825	22 AAC68428	Human hereditary h
4	10821.8	100.0	10825	22 AAC68427	Human hereditary h
5	10817	99.9	10825	22 AAC68427	Human hereditary h
6	10760.2	99.4	12146	21 AAA96794	Hereditary haemoch
c 7	10709	98.9	237326	19 AAV57903	Hereditary haemoch
c 8	3109	28.7	235033	19 AAV57926	Hereditary haemoch
9	1051.6	9.7	2506	21 AAA96769	cDNA sequence enco
10	1051.6	9.7	2727	19 AAV23525	Haemochromatosis q
11	517	4.8	517	22 AAC68441	Human hereditary h

ALIGNMENTS

RESULT 1

AAC68426

ID AAC68426 standard; DNA; 10825 BP.

XX AAC68426;

XX 21-FEB-2001 (first entry)

XX Human hereditary hemochromatosis 24d1 mutation DNA.

XX HH; hereditary hemochromatosis; chelation agent;

KW T-cell differentiation factor; iron overload; ds.

XX Homo sapiens.

XX US6140305-A.

XX 31-OCT-2000.

XX 04-APR-1997; 97US-0834497.

XX 04-APR-1996; 96US-0630912.

XX 16-APR-1996; 96US-0632673.

XX 23-MAY-1996; 96US-0652265.

XX (BIRA) BIO-RAD LAB INC.

XX Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK; Feder JN;

XX WPI; 2001-006341/01.

XX P-PSDB; AAB36870.

XX New hereditary hemochromatosis gene products or polypeptides, useful

Human hereditary h
Hereditary hemochr
Survivin gene. Ho
Human neuroblastom
Human neuroblastom
Human yesi gene.
Human CD39 like pr
Hereditary haemoch
Human hereditary h
Human hereditary h
PEDF full length s
PEDF full length s
Human hereditary h
Human hereditary h
Human PG-3 gene.
Human CD39 like pr
Human PG-3 gene.
Human glycosyl sul
Retinoblastoma bin
Partial human PGI
PGI genomic coding
Wild type PGI codi
Survivin gene. Ho
Human lipolysis st
Human lipolysis st
Human leptin fragm
Human hereditary h
Human hereditary h
Human hereditary h
Human hereditary h
Genomic DNA of a h
Hereditary haemoch
Human TBC-1 partia
Hereditary haemoch

PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload -
PS Disclosure; Fig 3; 108pp; English.
XX
CC The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene.
XX
SQ Sequence 10825 BP; 2999 A; 2253 C; 2647 G; 2926 T; 0 other;

Query Match 100.0%; Score 10825; DB 22; Length 10825;
Best Local Similarity 100.0%; Pred No. 0;
Matches 10825; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1501 CTACCTGTATCCACATTTTACACATGCAAGAATGAGGCATGGCAGCGCTGCTTCCTGG 1560
DB 1501 ctacgtgtatccacattttcacatgacaagaatgagggcatggcagcgctgctcctgg 1560
QY 1561 CAAATTTTATCAATGGTACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTTCATAGC 1620
DB 1561 caaattttatcaatggttacactgggcttgggtggcagagctcatgtctccacttcaagc 1620
QY 1621 TATGATTTCTTAAACATCACACTGCTATGAGGTTGAATTAATAAATTTTCATGTTGACAG 1680
DB 1621 tatgatttcttaaacatcacactgcattagaggttgaataataaaatttcatgttggagcag 1680
QY 1681 AAATATTTCATTGTTTACAAAGTGAATAGTCCGAGCCCATGTTTGACCTGTTCAAGGCC 1740
DB 1681 aaatatttcttatttacaagtgtaaaatgagtcacagccaatgtgtgcactgttcaagccc 1740
QY 1741 CAAGGGAGAGAGCAGGGAAACAAGTCTTTTACCCTTTTGCATTTTTCATGTTGAGGAGA 1800
DB 1741 caaggagagagagcagggaacaagctttaccctttgatattttgcatctctagtgaggaga 1800
QY 1801 GATGACAATAAGCAATGACGAGAAGATATACAACATCAGAAATCATGGGTGTTGTA 1860
DB 1801 gatgacaataagcaaatgagcagaagataacaacatcagggaatcatgggtgttgta 1860
QY 1861 GAAGCAGAGAAAGTCAGGGCAAGTCACTCTGGGCTGACACTTGAAGCAGACATGAAGGA 1920
DB 1861 gaagcagagagagtcagggcaagtcaactcgtgggtgacacttgagagagacatgaaagga 1920

QY	6301	AATGGTCTCCCCAGAGTAAAGTCTCTTAATTAACAAACATCTTCAGACACCTACTAT	6360	QY	7381	TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCCTTCATTTCTCTCCGTCACCTCAGAG	7440
Db	6301		6360	Db	7381		7440
QY	6361	TTTGGCAAGAGCTGTTAAGGTAGTACAGGGGCTTTGAGGTTGAGAAGTCACTGTGGCTAT	6420	QY	7441	ACATACACCTATGTCAATTTCCATTTCTTATTTTGGAGAGAGACTCCCTTAATTTGGGGGA	7500
Db	6361		6420	Db	7441		7500
QY	6421	TCTCAGAACCCAAATCTGGTAGGAATGAAATTTGATAGCAAGTAAATGTAGTTAAAGAAG	6480	QY	7501	CTTACATGATTCAATTTTAAACATCTCGAANAAGCTTTGAACCTCGGGACGTGGCTAGTCAT	7560
Db	6421		6480	Db	7501		7560
QY	6481	ACCCATGAGGTCTTAAAGCAGGAGGCAAGCAATGTCTAGGTTCTAAAGAAAGATG	6540	QY	7561	AACCTTACCAGATTTTACATGTATCTATGCAATTTCTGGACCCGTTCAACTTTTCCCT	7620
Db	6481		6540	Db	7561		7620
QY	6541	ATCACATTCAGCTGGGGATCAAGATAGAGCTTCTGGATCTTGAAGGAGAAGCTGGATPCCA	6600	QY	7621	TTGAATCTCTCTCTGTGTATCCCGAGTAACCTCATCTGTCCACCAAGCTTGGGATTTCTTC	7680
Db	6541		6600	Db	7621		7680
QY	6601	TTAGTGTAGGTTGAAGATGATGGGAGGTCTACACAGACGGAGCAACCATGCCAAGTAGGA	6660	QY	7681	CATCTGATGTGATGTGAGTTGACAGCTATGAAGGCTGTACACTGCACCAATGGGAAGAG	7740
Db	6601		6660	Db	7681		7740
QY	6661	GAGTATAAGGCATCTGGGAGATTAGAATAATTAATCTGTACTTTAACCCCTGAGTTTCGCT	6720	QY	7741	GCACCTGTCCAGAAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGGTGTTTTAGC	7800
Db	6661		6720	Db	7741		7800
QY	6721	AGTATPACTACCAATATGATGATTTTACCCCTGTGAACATCTGTGTGTGAGGAAAGA	6780	QY	7801	AGGTAGGAGGCAATATCTTGAAGGGGTTGTGAAGGGTGTGTAAGAGGTGTTTTTCTTAATTTGGCATGA	7860
Db	6721		6780	Db	7801		7860
QY	6781	GAATCAGAAAGAACGAGCTATACAGAGTCCCAAGGGTCTTTTGGGATATTGGGTATGA	6840	QY	7861	AGGTGTATACAGATTTGCAAAAGTTTAAATGTGCTCTCATTTGGGATGCTACTCTAGTAT	7920
Db	6781		6840	Db	7861		7920
QY	6841	TCAGTGGGTGTCTATTTGAAGGATCTTAAAGAGGAGGACCAGATCTCCCTTATATGGTG	6900	QY	7921	TCCAGACCTGGAAGATACAAATTAATTTTCTACCTGGTCTCTCTTGTGTGATTAATGAAA	7980
Db	6841		6900	Db	7921		7980
QY	6901	AATGTCTTCTTAAAGTTAGATGAGAGGTGAGGAGACCACTTAGAAGCCAAATAAGCAT	6960	QY	7981	ATTATGATAAGGATGATAAAAGCACTTACTTCTGTCGGACTCTCTGAGCACCCTACTTA	8040
Db	6901		6960	Db	7981		8040
QY	6961	TTCCAGATGAGAGATAATGGTTCTTTGAAATCCAAATAGTGCCACGCTCTAAATTTGAGATGG	7020	QY	8041	CATGATTTACTGCATGCACTTCTTACAAATATCTATGAGATAGGTACTATTTATPCCCAT	8100
Db	6961		7020	Db	8041		8100
QY	7021	GTCAATGAGGAAATTAAGCAGAGAGAGAGGCAAGATGCTGCTAGGTTTGTGATGCCCT	7080	QY	8101	TTCTTTTAAATGAAGAAAGTGAAGTAGGCGGCGGACGGTGGCTCAGCCTGTAAATCCC	8160
Db	7021		7080	Db	8101		8160
QY	7081	CTTCTCTGGGTCTTGTCTCCACAGGAGGAGCCATGGGGCACTACGTTCTTAGCTGAACG	7140	QY	8161	AGCAGCTTTGGGAGGCCAAAGCGGGTGGATCAGAGGTGAGAGATCGAGACCATCTCTGGC	8220
Db	7081		7140	Db	8161		8220
QY	7141	TGAGTACACGAGCAGCTGAGACTCAGTGTGGAGGAGAGCAAACTAGAGACTCAAGA	7200	QY	8221	TACATGTGTGAACCCCTCTCTTAATAAAATACAAAAATTAAGTGGCGTGGTGGCAG	8280
Db	7141		7200	Db	8221		8280
QY	7201	GGAGTGCATTTATGAGCTTCTTATGCTTTTACGAGAGAGATTGAACCTAAACATAGAAAT	7260	QY	8281	ACGCTTGTAGTCCCAGCTACTCGGAAGCTGAGCAGAGAAATGSCATGAACCCAGGAGG	8340
Db	7201		7260	Db	8281		8340
QY	7261	GCCTGACGAACTTCTTATGCTTTTACGCTTCTCTGTTCAATTTCCCTAAAGATTTCCCCAT	7320	QY	8341	CAGAGCTGCAGTGAGCCGAGTTTCCGCACTGCCTCCAGCTAGGTGACAGAGTGAAGA	8400
Db	7261		7320	Db	8341		8400
QY	7321	TTAGGTTTCTGAGTCTCTGCATGCCGGTGTATCCCTAGCTGTGACCTCTCCCTTGGAACTG	7380	QY	8401	CTCCATCTCAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATA	8460
Db	7321		7380	Db	8401		8460
QY	7381	TTAGGTTTCTGAGTCTCTGCATGCCGGTGTATCCCTAGCTGTGACCTCTCCCTTGGAACTG	7440	QY	8461	TAGATGATCTCATAGTTTCTGCTAGTGATGAACACAGGTTTCAAACTCAGTCAATCTGACCG	8520
Db	7381		7440	Db	8461		8520

Qy	10681	TGAGAGGTACAGGCCAAATCTTATGTGTATTAATTAATGTCACTATATAACTACTGT	10740			
Db	10681	Tgagaggtacagggccaaattcttctgtgtattataataatgtcatcttataactgt	10740			
Qy	10741	CAGTATTTTATAAAACATCTTTCAAACTACACACACATTTTAAAAACAAAACACACGTCTC	10800			
Db	10741	cagtattttataaaacattcttcaaaactcacacacatttaaaaaacaaacacigtctc	10800			
Qy	10801	TAAATCCCAAAATTTTCATAAAC	10825			
Db	10801	taaaatcccaaaatttttcataaac	10825			
RESULT 2						
ID	AAC68425 standard; DNA; 10825 BP.					
XX	XX AAC68425;					
XX	XX					
DT	21-FEB-2001 (first entry)					
DE	Human hereditary hemochromatosis DNA.					
DE	XX					
KW	HH; hereditary hemochromatosis; chelation agent;					
KW	T-cell differentiation factor; iron overload; ds.					
XX	Homo sapiens.					
XX	OS					
PN	US6140305-A.					
PN	XX					
PD	31-OCT-2000.					
XX	XX					
PF	04-APR-1997; 97US-0834497.					
XX	XX					
PR	04-APR-1996; 96US-0630912.					
PR	16-APR-1996; 96US-0632673.					
PR	23-MAY-1996; 96US-0652265.					
XX	XX					
PA	(BIRA) BIO-RAD LAB INC.					
XX	XX					
PI	Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;					
PI	Feder JN;					
XX	XX					
DR	WPI; 2001-006341/01.					
DR	P-PSDB; AAB36869.					
XX	XX					
PT	New hereditary hemochromatosis gene products or polypeptides, useful					
PT	for treating hereditary hemochromatosis in a patient, and as a metal					
PT	chelation agent alleviating iron overload -					
XX	XX					
PS	Disclosure; Fig 3; 108pp; English.					
XX	XX					
CC	The present invention relates to hereditary hemochromatosis gene					
CC	products. These proteins may be used to treat a patient diagnosed as					
CC	having human hemochromatosis disease. It is also useful as a metal					
CC	chelation agent or as a T-cell differentiation factor, and for					
CC	alleviating iron overload. They may also be used in protein replacement					
CC	therapy for individuals having a defective human hemochromatosis gene.					
XX	XX					
SQ	Sequence 10825 BP; 2998 A; 2253 C; 2648 G; 2926 T; 0 other;					
Query Match 100.0%; Score 10823.4; DB 22; Length 10825;						
Best Local Similarity 100.0%; Pred. No. 0;						
Matches 10824; Conservative 0; Mismatches 1; Indels 0; Gaps						
Qy	1	TCGAAGTGTGAGATAAAATTTTTTAAATGATGATTGAATTTTGAATAATCATAAATATTTA	60			
Db	1	tctaaagttgagatataaaattttttaaattgattggaatttttgaaataatcataattatta	60			
Qy	61	AATATCTAAGTTCAGATCAGACATGCGAAGCTACTTTCCCAATCAACACCCCT	120			
Db	61	aaataatcctaagttcagatcagacatgacgaagctactttcccaatcaaacacccct	120			

Db	61	aatactataagtttcagatcagacaattcggaagctactttcccacatacaacacccct	120
Qy	121	TCAGGATTTAAAAACCAAGGGGACACTCGATCACTAGTGTTTTCACAAGCAGGTACCTT	180
Db	121	tcaggatttaaaaccaaaggggacactggatcactagtgtttcacaagcagtaacctt	180
Qy	181	CTGCTGTAGGAGAGAGAACATAAGTTTCTGAAGACCCTGTGCTTTTCACCAGGAAGTT	240
Db	181	ctgctgtaggagagagaaactaaagtctctgaagacctgtgcttttcacagaagaagt	240
Qy	241	TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGTGACTTCTGGAGCCATCCCGG	300
Db	241	ttactggcatctcctgagcctaggcaatagctgtagggtgacttctgagccatccccg	300
Qy	301	TTTCCCGCCGCCCAAAAGACGGGAGATTTAACGGGACGTCGGCGGCAGAGCTGGGGAA	360
Db	301	tttcccgcccccacaaagaagcggagatttaacggggacgtcgggccagagactgggaa	360
Qy	361	ATGGGCCCGGAGCAGCGCGGGCTTCCTCCCTGATGCTTTTCAGACCGCGTCTCGT	420
Db	361	atgggcccgcgagccagcgcgctctctctctgctgtcttttgagacgcggtccgtg	420
Qy	421	CAGGGCGCTTTGCTGCGTGAGTCCGAGGBCTCGGGCGCAACTAGGGCGCGCGCGGGGTG	480
Db	421	caggggcgctgctgctgctgagtcagggctcgggcgaaactagggcgcgcggggggtg	480
Qy	481	GAAAAATCGAAATAGCTTTTCTTTGCGCTGGGAGTTTGCTAACTTTGGAGGACCTGC	540
Db	481	gaaaaacgaaactagctttct	540
Qy	541	TCAACCCATATCCGACAGCCCTCTCCCTACTTCTGCGTCCAGACCCGCTGAGGAGTGC	600
Db	541	tcaacctatccgcaagccctctccctactttctgctccagaccccgtagggaggtgc	600
Qy	601	CTACCACGTGAATGCAGATAGGGGTCCCTCGCGCCAGGACCTGCCCTCCCGCGCTGT	660
Db	601	ctaacctgaactgcagatagggtccctctcgccacaggacctgcgccctcccccggctgt	660
Qy	661	CCCGGCTCTCGGAGTGCATTTTGGAAACCGCCACCTCCCTCCGCCCACTAGATGCTTTT	720
Db	661	ccggctctgaggagtgacttttgaaacgcgccactcccttcccccaactagaatgctttt	720
Qy	721	TAAATAAATCTGTAGTTCCTACTGTAGCTGAGCTAAGCCTGGGGCTCTTTGAACCTGG	780
Db	721	taaaataactcgtagttctctcactttagctgagctaaagcctggggctccttgaacctgg	780
Qy	781	AACTCGGGTTTATTTCCAAATGTCAGCTGTGAGTTTTTTTCGCCAGTCACTCCAAACAGG	840
Db	781	aactcggggtttatttccaaatgtaagctgtgtagttttttccccagtcattctccaaacagg	840
Qy	841	AAGTTTTCCTTGAGTGTTCGCGAAGGCTGAGCAAAACCCACAGCAGGATCCGCACGG	900
Db	841	aagttctccctgagtcttgcgcgaagaaggtgagcaaacccacagcaggatccgcacagg	900
Qy	901	GGTTTCCACCTCAGACGAATGCTTGGCGGTGGGGCGCAAAAGATGGCGTGGGGA	960
Db	901	ggttttccacctcagaaacgaatcgctctgggcggctggggggcgaaagagtggcgcttg999ga	960
Qy	961	TCTGAATTTCTCACCAITCCACCACCTTTTGTGTGACCTGGGGGTCTCTAGGGT	1020
Db	961	tctgaattcttcaccattccaccacttttggtagacctgggggtggaggtctctaggggt	1020
Qy	1021	GGGAGGCTCTGAGAGAGGCTTACCTCGGGCCTTTCCCCACATCTTGGCAATTTGTTCTTTT	1080
Db	1021	gggaggctctgagagaggcctaccctcgggcctttcccactcttggcaattgttctctttt	1080
Qy	1081	GCCTTGGAAATTAAGTATATGTATTGTGAACGTTTGAACCGAACAATTCCTTTTCGG	1140
Db	1081	gcttggaaaattaaagtatagttagttttgaaagctttgaaactgaacaattctcttcttcgg	1140
Qy	1141	CTAGGCTTTATGTATTTGCATGTGCTGTGTAAATTAAGAGGCTCTCTACAAAGTACTGA	1200
Db	1141	ctaaggcttattgatttgcgaatgctgctgtaattaaaggcctctctcacaagtaactga	1200

Db 3361 ||||| 3420
QY 3421 TCTAATTTGCCGTGAGCCCAACTCCTGAGTTCAACTACCATGCTGACACACACTTAAC 3480
Db 3421 tctaatttgccctgagacccaactcctgagtccaactaccatggtctgagacacaccttaac 3480
QY 3481 ATTTCCTAGATCCACAGCTTTAGTGAGTCTGTCTTAATCATGAGTATTGGAAATAGGAT 3540
Db 3481 attttctagaatccaccagcttttagtgagctgtcttaatcatgagtattggaataagat 3540
QY 3541 CTGGGGGAGTGAGGGGTGCGAGCCAGCTGTGCAGAGAAAGACACACAGGAAAGAGC 3600
Db 3541 ctggygggcagtgaggyggcgagccagctgtgagagagaaagacacagaggaagc 3600
QY 3601 ACCCAGGACTGTCTATATGGAAGAAAGACAGACTGCAACTCACCTCTTACAAAAATGAGGA 3660
Db 3601 acccaggaactgtcataatggaagaaagacagactgcaactcaccttcacaaaatgagga 3660
QY 3661 CCAGACACAGCTGATGGTATGAGTTGATGCAGGTGTGTGGAGCCTCAACATCCTGCTCCC 3720
Db 3661 ccagacacagctgatggatgagttgatgcagggtgtgtggagcctcaacatcctgtctcc 3720
QY 3721 CTCTACTACACATGGTTAAGCCTGTTCCTGTCTCCAGGTTACACTCTCTGCACTA 3780
Db 3721 ctctactacacatggttaagcctgtgtctgtctccagggttcacactctctgcacta 3780
QY 3781 CCTCTTATGAGGTGCCTCAGACGAGGACCTTGGTCTTTCCTTGTGTTGAAGCTTTGGGCTA 3840
Db 3781 cctctctatggtgctcagagcaggaaccttggctcttctctgtttgaagcctttgggcta 3840
QY 3841 CGTGGATCACCAGCTGTTCGTGTTCTATGATCATGAGATCGCGTGTGGAGCCCCGAAC 3900
Db 3841 cgtggatgaccagctgttcgtgtctatgatcatgagatgcgcgtgtggagcccccgaac 3900
QY 3901 TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGCTGCAGCTGAGTCAGAGTCGAA 3960
Db 3901 tccatgggtttccagtagaatttcaagccagatgtgctgcagctgagtcagagctctgaa 3960
QY 3961 AGGTGGGATCACATGTTCACTGTGTGACTTGTGACTATATGGAANAATCACACACAG 4020
Db 3961 aggttgggatcacatgttctactgttgacttggactattatggaaaatcacaccacag 4020
QY 4021 CAAGGATATGTGGAGAGGGGCCCTCACCTTCCTGAGCTGTGCAGAGCTTTTCATCTTTC 4080
Db 4021 caaggatgtggygagaggyggccctccctctcaggtgtgagagcttctcatctttc 4080
QY 4081 ATGCATCTTGAAGAAACAGCTGGAAGTCTGAGGTCTTGTGGAGCAGGGAAGAGGAA 4140
Db 4081 atgcatcttgaagaaacagctggaagtctgaggtcttgtggagcaggaagaggygaag 4140
QY 4141 GAATTTGCTTCTCAGATCATTTGGTCTTGGGATGGTGGAAATAGGGACCTATTCCCTT 4200
Db 4141 gaatttgcctctgagatcattttggctcttggggtgtggatggtggaataaggagcctattcctt 4200
QY 4201 TGGTTGAGTTAAACAGCTGGGATTTTCCAGATGCCACACCCCTGCAGAGTCATCCCTG 4260
Db 4201 tggttgagttaaacaagcttggggtattttccagagtcaccacccctgcaggtcatacctg 4260
QY 4261 GGCTGTGAATGCAAGAGAACACAGTACCGAGGCTTACTCGAAGTACGGGTATGATGGG 4320
Db 4261 ggctgtgaattgcaagagacaacagtcaccagggctacttggagtaacgggtatgatggg 4320
QY 4321 CAGACACCCTTGAATTTCTGCCCTGACACACTGGATTGGAGACAGAGAACCCAGGGCC 4380
Db 4321 caggaaccaccttgaattctgtccctgcacactggtattggagagcaggaaccaggggcc 4380
QY 4381 TGGCCCCAACAGCTGGAGTGGGAAAGGCACAAAGATTCGGGCCAGGACAGAGGCCCTAC 4440
Db 4381 tggcccccaagcttggagtggygaaagacaagattcggccagggcagaaacagggctac 4440
QY 4441 CTGAGAGGGACTGCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGAGAGGTGTTTTG 4500
Db |||||

Db 4441 ctggagagggaactgccctgcacagctgcagcagttgctgagagctggggagaggtgttttg 4500
QY 4501 GACCAACAAGGTATGTGGGAAACACACTTCTGCCCCCTATACTCTAGTGGCAGAGTGGAGG 4560
Db 4501 gaccacaaggtatggtggaaacacacctctgccctatactctagtggcagagtggagg 4560
QY 4561 AGGTTGAGGGCAGCGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGCCCTC 4620
Db 4561 aggttgcagggcaacggaatcccttgggttgcagagtttcagagagtgctggtgctcc 4620
QY 4621 TCCAAATCTCTGGGAAGGAGCTTTCTCAATCCTAGAGTCTCTACCTTATATTAATTGAGATGA 4680
Db 4621 tccaaattctgggaagggaactttctcaactcctagagtctctacctataatigagatgta 4680
QY 4681 TGAGACAGCCACAAGTCATGGGTTTAATTTCTTTTCTCCATGCATATGCTCAAGGGAA 4740
Db 4681 tgagacagccacaagtcaggggttaatttctctctctccatgcatacgtggtcaaaaggaa 4740
QY 4741 GTGCTATGCCCCCTTCTTTTATTAAACCAATAATCTTTTGTATATTATACCTCTTAA 4800
Db 4741 gtgtcatgccccctgtcttttatttaaccaataaactctttgtatatattataacctgttaa 4800
QY 4801 AAATTTCAGAAATGTCAGGCCGGGACGGTGGCTCACCCCTGTAAATCCAGACACTTTGGG 4860
Db 4801 aaatttcagaaatgtcaaggccggcagcgtggctcaccctgttaatccccagcaccttggg 4860
QY 4861 AGCCGAGGCGGGTGTCTCAAGGTCAGGAGTTTGAGACCAGCTGACCAACATGTTGAA 4920
Db 4861 agccagagcgggtgtgtcaaaaggttcagaggttttgagaccagcctgaccacaatggtgaa 4920
QY 4921 ACCGCTCTCTAAAAAATACAAAAATTAGTGGTCAAGTCATGCGCACCTGTAGTCCCA 4980
Db 4921 acccgctctctaaaaaatacaaaaaattagctggttcacagtcacgtgacacctgtagccca 4980
QY 4981 GCTAATTTGGAAGCTGAGGACGAGGATCGCTTGAACTTGGGAAGGGAGTTGCACCTGA 5040
Db 4981 gctaaattggaaagctgagcgagagcatcgcttgaacctgggaagcggaagttgcactga 5040
QY 5041 GCCAAGTCGGCCACTGCACCTCCAGCTTAGGCAGCAGAGTGTAGACTCCATCTTAAAAA 5100
Db 5041 gccaaagtgcgcccactgcactccagccttaggcagcagagtgagacctccatcttaaaaa 5100
QY 5101 AAAAAAATAAAGAAATTCAGAGATCTCAGCTATCATATGAATPACAGGACACAA 5160
Db 5101 aaaaaaataaagaaagaaattcagagatctcagctatcatatgaataccaggacaaa 5160
QY 5161 ATATTAAGTGAGGCCACTTATCAGAGTGAAGAACCTTTAGGTTAAAGTTTCTTTTCA 5220
Db 5161 atatcaagtgaagccactcatcagagtagaagaatcccttaggttaaaagttcttctcat 5220
QY 5221 AGAACATAGCAATAATCACTGAAGCTTACCTATCTTTACAAAGTCGGCTTCTTATAACAATGC 5280
Db 5221 agaacaatgaataataactcactgaagctacctaacttacaagtcgcgctctctataacaaatgc 5280
QY 5281 CTCCTAGGTTGACCCAGGTGAACCTGACCATCTGTATTCAAATCAATTTCAATGCAATAA 5340
Db 5281 ctcctaggttgaccagggtgaacctgacatctgtattcaatcattttcaatgacataa 5340
QY 5341 AGGGCAATTTTATCTATCAGAAACAAAGAACATGGGTACAGATATGTATTTATATGATG 5400
Db 5341 agggcaattttattctatctatcagaacaagaacatgggtaacagatatgtatatattcatgtg 5400
QY 5401 AGGAGAACAGCTGATCTGACTGCTCTCCAAGTGACACTGTGTTAGAGTCCCAATCTTAGG 5460
Db 5401 aggagaacaagctgactgactgctctccaaagtgcactgtgttagagttccaaactttagg 5460
QY 5461 ACACAAAATGGTGTCTCTCTAGTGTGTTGTTTTTCTGAAAAGGGTATTTCTTTCCTCC 5520
Db 5461 acacaaaatgggtctctctctgtagctgtttttttcttgaaaaggggtatttcttctccccc 5520
QY 5521 AACCTATAGAAGGAGTGAAGTTCCAGTCTTCCTGGCAAGGGTAAACAGATCCCTCTC 5580
Db 5521 aacctatagaaggaagtgaagttccagttcttccctgggaagggtaaacagatccctctc 5580

QY 9961 CATTTCTGAAGCATATGACAAATTTATTTCTCTCTTAATATCTTACTATATCTGAAAGCAGA 10020
|||||
Db 9961 catctgaagcatatgacaaattattctcttcttaatactcttactatactgaagcaga 10020
QY 10021 CTGCTATAAGGCTTCACCTTACTCTCTTACCTCATAGAAGTAATGTTACAATTAATTTATT 10080
|||||
Db 10021 ctgctataaggcttcactctactctctacotcataaggaatatgttacaattattatt 10080
QY 10081 AGSTAAGCATTTGTTTATATTTGTTTATTTTACCTGGGCTGAGATTTTCAAGAAACACC 10140
|||||
Db 10081 agstaagcattgttttataattggttttattttcaccctgggctgagatttccaagaacacc 10140
QY 10141 CCAGTCTTCACAGTAACACATTTTACCTAACACATTTTACTAAACATCAGCAACTGTGSCCT 10200
|||||
Db 10141 ccagtcttcacagtaacacatttcactaacacatttactaaacatcagcaactgtggcct 10200
QY 10201 GTTAAATTTTTTAATAGAAATTTTAAAGTCTCATTTTCTTCGGTGTTTTAAAGCTTAA 10260
|||||
Db 10201 gttaatTTTTtaataagaaatttttaagctctcatTTTCTTCGGTGTTTTtaagcttaa 10260
QY 10261 TTTTCTGGCTTTATTCATAAATTTCTTAAGGTCAACTACATTTTGAATAATCAAGACCTG 10320
|||||
Db 10261 ttttctggctttattcataaattcttaaggtcaactacatttgaaataatccaagacctg 10320
QY 10321 CATTTTAAATTTTATTCACCTCTGGCAAAACCATTCACAAACCATGGTAGTAAAGAGAA 10380
|||||
Db 10321 cattttaaattcttattcacctctggcaaacatttcacaaacccatggtagtaagagaa 10380
QY 10381 GGGTGACACCTGGGCGCATAGGTAATGTAACACCGTGTCCGGTACCAGAGATGTCAG 10440
|||||
Db 10381 gggtgacacctggcgccataggttaaattgtaacacggtgtccggtaaccagagatgycag 10440
QY 10441 CGCTGAGGGTTTCTCCTGAAGGTAAGGAATAAAGAAATGGGTGGAGGGCGTGCACTGGAA 10500
|||||
Db 10441 cgctgagggtttctcctgaaggtaaggaataaagaaatgggtggaggggcgctgcaactggaa 10500
QY 10501 ATCACTTGTAGAGAAAAGCCCTGAAATTTTGAGAAAACAAAGAACTACTTACCAG 10560
|||||
Db 10501 atcacttgtagagaaaagccctgaaatttgagaaaacaaagaaactacttaccag 10560
QY 10561 CTATTTGAATTTGCTGGAATCACAGGCCATTTGCTGAGCTGCTGAACCTGGGAACACAAAC 10620
|||||
Db 10561 ctatttgaattgctggaaatcacagccctctgctgagctgctgaactgggaacacaaacag 10620
QY 10621 AAGGAAACAAACCACTCTGATATATCTAGTCAAGTACAGCAGGTGATGAGGACTGC 10680
|||||
Db 10621 aaggaaacaaacacctctgataatcatgagtcgaagtacagcaggtgattgaggactgc 10680
QY 10681 TGACAGGTACAGGCCAAATTTCTTTATGTTGTATTAATTAATGTCATCTTTAATTAATCTGT 10740
|||||
Db 10681 tgagaggtacagggccaaattcttatgttgattataataatgcatcttataatactgt 10740
QY 10741 CAGTATTTTATAAACAATTTCTCAACAATTCACACACATTTTAAACAAACAACTGTCTC 10800
|||||
Db 10741 cagtattttataaacaattcttcaacaactcacacacatttataaacaacaaactgtctc 10800
QY 10801 TAAATCCCCAAATTTTTCATAAAC 10825
|||||
Db 10801 taaatccccaaatttttataaac 10825

RESULT 3

AAC68428
ID AAC68428 standard; DNA; 10825 BP.
AC AAC68428;
XX AAC68428;
XX 21-FEB-2001 (first entry)
DT Human hereditary hemochromatosis 24d1/2 mutation DNA.
XX HH; hereditary hemochromatosis; chelation agent;

KW T-cell differentiation factor; iron overload; ds.
XX Homo sapiens.
OS US6140305-A.
PN 31-OCT-2000.
XX 04-APR-1997; 97US-0834497.
XX 04-APR-1996; 96US-0630912.
PR 16-APR-1996; 96US-0632673.
PR 23-MAY-1996; 96US-0652265.
XX (BIRA) BIO-RAD LAB INC.
XX Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK,
PI Feder JN;
XX WPI; 2001-006341/01.
DR P-PSDB; AAB36872.
XX New hereditary hemochromatosis gene products or polypeptides, useful
PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload -
XX Disclosure; Fig 3; 108pp; English.
XX The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene.
XX Sequence 10825 BP; 2999 A; 2252 C; 2648 G; 2926 T; 0 other;

Query Match 100.0%; Score 10823.4; DB 22; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10824; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTTAGGTTGACATAAAATTTTAAATGTATCATTTTGAATAATCAATAATATTTA 60
|||||
Db 1 tctaaggttgagataaaattttaaattgatgatgaaatttgaaaaataataatttta 60
QY 61 AATATCTAAAGTTTCAGATCAGAACATTTGGAAAGCTACTTTCCCAATCAACAAACCCCT 120
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Db 61 aatatctaagttcagatcagaaacattcggaagctactttccccaatcaacaacacct 120
QY 121 TCAGGATTTAAACCAAGGGGACACTGGATCACCTAGTGTTCACAGAGGTACCTT 180
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Db 121 tcaggattttaaacaacaaaggggacactggatcacctagttttcacaaagcaggtacctt 180
QY 181 CACCTGTAGAGAGAGAGAACTAAAGTTCTGAAAGACCTGTTGCTTTTCCACGAGAAGTT 240
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Db 181 ctgctgtaggagagagagaactaaagttctgaaagacctgtgtctttccaccaggaagt 240
QY 241 TTAGTGGCATCTCTGAGCCCTAGGCAATAGCTGTAGGCTGACTTCTGGAGCATCCCG 300
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Db 241 ttaactggcatctctcctgagcctagcaatagctgtaggtgacttctggagccatccccg 300
QY 301 TTTCCCGCCGCCCAAAAGAGGAGATTTAACGGGACGTGCGGGCAGAGCTGGGAA 360
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Db 301 tttccccgcccccaaaagagagatttaacggggagctgcggccagagctgggaa 360
QY 361 ATGGGCGCGGAGCCAGCGCGGCTTCTCCCTCTGATGCTTTTTCACACCGCGTCTCG 420
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Db 361 atggggcccgcgagcgagggcgcttctccctctctgagcttcttgacacgcgcgctcg 420
QY 421 CAGGGCGCTTGTGCGTGTAGTCCGAGGGCTCGGGCGCAACTAGGGGCGCGCGGGGTG 480
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Db 421 cagggcgcttgtcgtcgtgagcccgagggcgctgcggcgaaactagggcgcgcgggggtg 480

QY 481 GAAAAATCGAAACTAGCTTTTCTTTTGGCTTGGAGTTTGCTAACTTTGGAGACCTGC 540
DB 481 gaaaaatcgaaactagctttttcttttggcttggagtttgctaactttggaggacctgc 540
QY 541 TCAACCCATCCGGAAGCCCTCTCCCTACTCTTCTGCTCGCAGACCCCGTGAGGAGTGC 600
DB 541 tcAaCCcAtCcGgAaGcCcCtCcCtAcTcTtGcTcGcTcGcAgAcCcCcGtGagGgAgTgc 600
QY 601 CTACCACCTGAAGTGCAGATAGGGTCCCTCGCCCGCAGACACTGCCCTCCCGGCTGT 660
DB 601 ctaccactgaagtcagataggggtccctcgcgccagagacctgcctccctcccgcgctgt 660
QY 661 CCCGGCTCTGGAGTGACTTTTGAACCGCCCACTCCCTTCCGCCCACTAGAATGCTTT 720
DB 661 cccggctctgcggagtgcacttttggaaacgcccactccctcccccaactagaatgcttt 720
QY 721 TAAATAATTCGTAGTTCCTTCACCTTGAGCTGAGCTAGACCTGGGGCTCTTGAACTGG 780
DB 721 taaataaatTCGTAGTTCcTTCaCCTTGaGCTGaGCTAGaCCTGGGGCTCTTGAAcTGG 780
QY 781 AACTCGGGTTTATTTCCAAATGTCACTGTGCAGTGTGCTTTTCCCACTATCTCCAAACAGG 840
DB 781 aactcgggtttatttccaaatgtcagctgcagttttttcccaagtcatctccaaacagg 840
QY 841 AAGTTCCTCCCTGAGTGTGCTCCGGAAGGCTGAGCAAAACACAGCAGGATCCGACGG 900
DB 841 aagttcttccctgagtgtctgcgagaaggctgagcaaaaccacagcaggatccgcacgg 900
QY 901 GGTTCCTCACTCAGAACCAATGCTGGCGGTGGGGCGGGAAGAGTGGCGTTGGGA 960
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QY 1021 GGGAGGCTCTGAGAGAGGCTACTCGGGGCTTTCCCACTCTTGGCAATGTGCTCTTT 1080
DB 1021 gggaggtcctgagagagagctactcgggctttcccaactcttggcaattgttctttt 1080
QY 1081 GCGTGGAAAAATTAAGTATATGTAGTTTGAACGTTTGAACCTGAACATCTCTTTTCGG 1140
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QY 1141 CTAGCGTTTATGATTTGCAATGCTGTGTAATTAAGAGCCCTCTCTACAAAGTACTGA 1200
DB 1141 ctaggctttattgattgccaatgctgtgtaattaaagaggcctctacaaaactcta 1200
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DB 1201 taatgaacatgtagcaatgcaactctcttaagttacattcatctgatctcttattga 1260
QY 1261 TTTTCACTTAGGCATAGGGAGGTAGGAGTAATAATACGTTTATTTTACTAGAAGTTAACT 1320
DB 1261 ttttcaactaggcataaggaggtagagctaataacgtttattttactagaagtttaact 1320
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DB 1321 ggaattcagattataactcttttcaagtttacaagaacaataaataatctggttttctg 1380
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DB 1381 atgttatttcaagtactacagctgctctctaacttagtttagacagtgtatttgccctgag 1440
QY 1441 TGTAGCAGGTGTTCTGTGGGTACAGCCGGCTCTAGCAGACAGCACACTTTGAGTTTTCGTA 1500
DB 1441 tgtagcagagtggtctgtgggtcaacgcgcgcctcagcacagcacttttagtcttggta 1500
QY 1501 CTACGTGTATCCAAATTTTACATGACAAAGAATGAGGCATGGCAGCCGCTGCTTCCTGG 1560
DB 1501 ctacgtgtatccaatTTTAcATGaCAAGAAATGaGGCATGGCaGCCGCTGCTTCCTGG 1560

QY 1561 CAAATTTATTCAATGTGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTTCATAGC 1620
DB 1561 caaatTTATTCAaTGTGTAcACTGGGCTTTgGTgGcAGAGcTcATGTCTCCaCTTTCaTAGc 1620
QY 1621 TATGATTTTAAACATCACACTGCATTAGAGTTTGATAATAAAATTTTCATGTTGAGCAG 1680
DB 1621 tatgattcttAaaCaTcAcAcTgCAtTAGagTTtGaTaATAaaATtTCaTgTTGaGCaG 1680
QY 1681 AAATATTTCATTTGTTTACAGTGTAAATGACTCCAGCCATGTGTGCACGTGTTCAAGCCC 1740
DB 1681 aaatattcattgtttacaagttaaatgagtcaccagccaTgtgtgcactgtttcaagccc 1740
QY 1741 CAAGGGAGAGCAGGAGGAAACAAGTCTTTTCCCTTTTGATATTTTGATCTTACTGCGGAGA 1800
DB 1741 caagggaagagcagggaaacaagctcttaccctttgataatttgcattcttagtgggaga 1800
QY 1801 GATGACAATTAAGCAATGAGCAAGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA 1860
DB 1801 gatgacaataagcaaaTgagcagaagaGataacaacatcaggaaatcatgggtgtgtga 1860
QY 1861 GAAGCAGAGAAGTCAAGGCAAGTCACTCTCGGGCTGACACTTCAGCAGACACATGAGGA 1920
DB 1861 gaagcagagaagtcaggggcaagtcactctgggctgaccttgagcacttgagcagacatgaagg 1920
QY 1921 AATAAGAATGATATTGACTGGGAGCAGTATTTCAGGCAAACTGAGTGGGCTGCGAAG 1980
DB 1921 aataagaatgatattgactgggagcagattttcccagggaactgagtggtgggctggcag 1980
QY 1981 TTGGATTTAAAGCGGTTTTCACGACTACTCATGTGTGTGTGTGTGTGGGGGGGGGG 2040
DB 1981 ttggattaaaagcgggttttctcagcaactactcatgtgtgtgtgtgtgtgggggggggg 2040
QY 2041 CGCGTGGGGGTGGGAAGGGGACTACCACTCTCANTGAGGATGCTAGCAGTATCCTGT 2100
DB 2041 cggcgtgggggtgggaagggggactaccatctgcatgtaggatgtctagcagtatctctgt 2100
QY 2101 CTCCCTACTACTAGTGTCTAGGAGCAGCTCCCGGCTGAGTGTGACACCAAAATGCTCT 2160
DB 2101 cctccctactcaatagtgctaggagcactccccagctcttgacaacccaaaatgtctct 2160
QY 2161 AAACCTTGCCACATGTCACCTAGTAGACAAACTCTCTGGTTTGAAGACTCGGTTGAAAA 2220
DB 2161 aaacttgccacatgtcactagtagacaaactcctggttaagaagctcgggttgaaaaa 2220
QY 2221 AATAAACAAGTAGTGTGGGAGTAGAGCCAAAGAGTAGTAACTGGCTCAGAACAGGA 2280
DB 2221 aataaacaagtagtgctgggagtagagccaaagaagtaggtaagtgggctcagaagagga 2280
QY 2281 GCCACAAACAAGTTGTGAGGGCGCTGTAGGCTGTGGTGTGAATTTCTAGCCAAGGAGTA 2340
DB 2281 gccacaaaagttgtgcaggcgcctgtaggctgtggtgtggaattcttagccaagagta 2340
QY 2341 ACAGTGTATCTGTACAGGCTTTTAAAGATTGCTCTGGCTGTATGTGGAAGCAGAAATG 2400
DB 2341 acagtgtatctgtcacaggcttttaaagattgtctgtgctgtatgtggaagcagaatg 2400
QY 2401 AAGGAGCAACAGTATAAAGCAGGGAGCCCGCAGGAAAGCTGTTACACAGTCCAGGCAAG 2460
DB 2401 aaggagcaacagtaaaagcaggaggaccccgccaggaaagctgttacacagtcacaggcaag 2460
QY 2461 AGTGTAGTGGTGGGTGGGAAACAGAAAGAGGAGTGACAAACCAATGTCTCTCTGAA 2520
DB 2461 aggtagtggagtgggctgggtgggaacagaaaggagtgacaaaaccattgtctctctgaa 2520
QY 2521 TATATTTCTGAAGGAAGTTGCTGAAGGATTTCTATGTGTGTGAGAGAAAGAGAAATTTGG 2580
DB 2521 tatattctgaaggaagtgtctgaaggattctatgtgtgtgagagaaaagagaagaattgg 2580
QY 2581 CTGGGTGTAGTAGCTCATGCCAAGGAGGAGGCCAAGGAGCAGAGATTCCTGAGCTCAGGA 2640
DB 2581 ctgggtgttagtagtcatgccaaaggagaggccaaaggagagcagattcctcgagctcagga 2640
QY 2641 GTTCAAGACCGCCTGGGCAACACAGCAAAACCCCTTCTTACAAAAAATACAAAAATTA 2700

Qy	4861	AGCCGAGGCGGGTGTCTACAAGGTCAGAGTTTGAGACCAAGCCTGACCAACATGPTGGAA		4920
Db	4861	agccgagggcggtgtgtcacaaggctcaggaggtttgagaccagcgtgaccaacatcggtgaa		4920
Qy	4921	ACCCGTCCTTAAAAAATACAAAATTAGCTGGTCACAGTTCATGCGCACACTGTAGTCCCA		4980
Db	4921	accgctcttaaaaaatacaaaaattagctggtcacagtcacatgcgcaacctgtagtccca		4980
Qy	4981	GCTAATTTGAAGGCTGAGCGAGAGCATCGCTTGAACTGGGAAGCGAAGTTGCACATGA		5040
Db	4981	gctaattggaaagctgagcgaggagcatcgctgaacctgggaagcggaagtgtgactga		5040
Qy	5041	GCCAAGATCGGCCACTGCACCTCCAGCCTAGGCAGCAGGTGAGACTCCATCTTAAAAAA		5100
Db	5041	gccaaagtgcgccactgcactccagctaggcgagcagcaggtgagactccatcttaaaaaa		5100
Qy	5101	AAAAAANAANAAGAAATTCAGAGATCTCAGCTATCATATGATTAATACCAGGACAAA		5160
Db	5101	aaaaaanaanaaagaataatcagagatctcagctatcatatgaataccaggacaaa		5160
Qy	5161	ATATCAAGTGAAGCCACTTATCAGAGTAGAAGATCCCTTAGGTTAAAAAGTTCTTTTCAT		5220
Db	5161	atatcaagtgaagccacttatcagagtagagaaatccctttaggtttaaagttcttttcat		5220
Qy	5221	AGAACATAGCAATAATCTAGAGTACCTATCTTTACAAGTCCGCTCTTTATTAACAATGC		5280
Db	5221	agaacatagcaataatctactgaagctactatcttacaagtcgctcttttataacaatgc		5280
Qy	5281	CTCTAGGTTGACCCAGGTAACCTGACCATCTGATTCAATCATTTTCATGCACATAA		5340
Db	5281	ctctaggttgacccagggtgaaacttgacaactctgtatccaactatttcaatgacataa		5340
Qy	5341	AGGGCAATTTTATCTATCAGAAACAAGAACATGGGTAAACAGATGATATTTACATGTG		5400
Db	5341	agggcaattttatctatcagaaaaagaacatgggttaacagatgatgatatttacaatgtg		5400
Qy	5401	AGGAGAACAGCTGATCTGACTGCTCCAGTGCACACTGTTGTAGAGTCCCAATCTTAGG		5460
Db	5401	aggagacaagctgatactgactgctccagctgacactggtttagagttcccaatctcagg		5460
Qy	5461	ACAAAAATGGTGCTCTCCTGTAGCTGTGTTTTCTGAAAAGGGTATTTCCCTTCCTCC		5520
Db	5461	acaaaaatggtgtctctctctgtagctgtgtttttctgaaaagggattttctctctcc		5520
Qy	5521	AACTATAGAAAGAGTGAAGTTCAGTCTTCGTCGCAAGGGTAAACAGATCCCTCTC		5580
Db	5521	aaactatagaaggaagctgaagtccagctctctctcggcaagggttaaacagatccccctc		5580
Qy	5581	CTCATCTTCCTCTTTCTGTCAAGTGCCTCTCTTGGTGAAGGTGACACATCATGTGACC		5640
Db	5581	ctcatcttctcttctgtcaagtgcctcttctgttgaaggtgacacatcatgtgacc		5640
Qy	5641	TCATCTAGCACCTACTAGGGTCTGGGCTTGAACTACTACCCCCAGAACATCACCATTG		5700
Db	5641	tctcagtgaccactctacggtcgtcgggccttgaaactactaccocccagaaacatcaccatg		5700
Qy	5701	AACTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGAGTTCGAACCTTAAGACAGTATTG		5760
Db	5701	aagtggctgaaggataaagcagccaatggatgccaaagggttcgaaacctaaagacgtattg		5760
Qy	5761	CCCAATGGGATGGGACCTTACCAGGCGTGGATAACCTTGGCTGTACCCCTGGGGAGAG		5820
Db	5761	cccaaagggtatgggacctaccagggctggataaacttggctgtaccocctggggaagag		5820
Qy	5821	CAGAGATATACGTACCAAGGTGGAGCACCCAGGCCCTGGATCAGCCCCCTCATTTGATCTGG		5880
Db	5821	cagagataatcgtlaaccaggtggaacaccagccctggatcagccccctcattgtgactcgtg		5880
Qy	5881	GGTATGTACTGATGAGAGCCAGGACCTGAGAAAATCTATTGGGGGTTGAGAGAGTGC		5940
Db	5881	ggatgtgactgatgagccagagagctgagaaatctattgggggttgagagagtgccc		5940

QY	5941	tgagagaggttaattatngccactgagatgagatctgctctttttttaggggggtgggctgagg	6000
Db	5941	tgaggaggttaattatdgccagtgagatgagatctctctcttgttaggggggtgggctgagg	6000
QY	6001	gtgccaatcaaaagcgtttaacttgcgttttttgcgtttttttagagccctcaccgttgcacccc	6060
Db	6001	gtgccaatcaaaagcgtttaacttgcgttttttgcgtttttttagagccctcaccgttgcacccc	6060
QY	6061	tagtcaatttgagtcntcagttggaaattgcctgttttttgcgtcaattttgttcatttggaaattt	6120
Db	6061	tagtcaatttgagtcntcagttggaaattgcctgttttttgcgtcaattttgttcatttggaaattt	6120
QY	6121	tgttcataaatttaaggaagagcaggggttcaagtgcagttagaacaagggggaagtcctct	6180
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QY	6181	tagttacctctgccccagggcacactgggaagaggggcagagggggtcgtgcacatcagggg	6240
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QY	6241	aagcattttctcatttatattctttggggcacaccagcagctccctggygagacagaaat	6300
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QY	6301	aatgggtctccccagatgaagctctaatctacaacaactcttcagagcaccctactat	6360
Db	6301	aatgggtctccccagatgaagctctaatctacaacaactcttcagagcaccctactat	6360
QY	6361	tttccaaagactggtttaaggtagtacaggggctttgaggttgagaagtcactgttggaag	6420
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QY	6421	tctcagaacccaattcgttagggatgaattgatacagaactaaatctagcttaaagaag	6480
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QY	6661	gagtaataaggcatactcggagattagaaataattactgtaccttaacctgagtttgggt	6720
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Db	6721	agcttatcactcaccattatgcatatttaccctcctgaacatctgtgtgtgtagggaaaaa	6780
QY	6781	gaattcagaagaagccagctcatcacaggtcccaagggctttttgggattttgggttatga	6840
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QY	6841	tcacttgggggtctcattgaaagattccttaagaaaggagaccagatctccctttatgtgtg	6900
Db	6841	tcacttgggggtctcattgaaagattccttaagaaaggagaccagatctccctttatgtgtg	6900
QY	6901	aattgtgttttaagaactttagatgcagaggtgagagaccagtttagaaagccaataagcat	6960
Db	6901	aattgtgttttaagaactttagatgcagaggtgagagaccagtttagaaagccaataagcat	6960
QY	6961	ttccagatgcagatattggttcttgaaatcccaattagtcgccaggtctaaattgagatgg	7020
Db	6961	ttccagatgcagatattggttcttgaaatcccaattagtcgccaggtctaaattgagatgg	7020
QY	7021	gtgaattgaggaaaaataaggaaagagagaaggaagcagatggtgccttaggttttgtgatgctt	7080

|||||
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Db 7921 tccagacctgaaagaa tcaaa taatttttaactactgtctctcctgttctgtctgataatgaaa 7980
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QY 8041 CATGCATTACTGCATCCTCTTACAAATTTCTATGATAGATGATCTATTATCCCAT 8100
Db 8041 catgcattactgcatcctctctcaaa taattctatgagaa taggtaccattatcccat 8100
QY 8101 TTCTTTTTTAATGAAGAAAGTGAAGTAGCGGGGACGCTGCTCACGCCCTGTAAATCCC 8160
|||||

Db 8101 ttcttttttaaatgaagaaagtgaagtaggcccgggacaggtgggtccacgcgctgtaatccc 8160
QY 8161 AGCACTTTGGGAGGCCAAAGGGGTGATCAGAGGTGAGAGATCGAGACCATCTCGC 8220
Db 8161 agcacttttgggaggccaaaggggtggatcacagaggtcagagatcgagaccatccctggc 8220
QY 8221 TAACATGTTGAAACCCCATCTCTAATAAAAAATACAAAAATTAGCTGGCGGTGGTGGCAG 8280
Db 8221 taacatggtgaaaccccatctctaataaaaaatacaaaaaatttagctggcgtgggtggcag 8280
QY 8281 AGCCCTGTAGTCCCAGCTACTCGGAAGCTGAGCAGGAGAGATGGCATGAACCCAGGAGG 8340
Db 8281 agccctgtagttcccagctactcgggaaggtgagcagagaaatgagca tgaaccccagggagg 8340
QY 8341 CAGAGCTTCCAGTGGCCGAGTTTGGCCACTGCATCTCAGCCTAGGTAGTGCACAGAGTGAGA 8400
Db 8341 cagagcttcagtgagcggagtttggccactgcactccagcctaggtgcagagatgaga 8400
QY 8401 CTCCTATCTCAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAGTCAAGTA 8460
Db 8401 ctccatctcaaaaaataaaaaataaaaaataaaaaataaaaaataaaaaataaagtgaagta 8460
QY 8461 TAGAGTATCTCATAGTTTGTCTAGTGATAGAAAACAGGTTTCAAACTCAGTCAATCTGACCG 8520
Db 8461 tagagtatctcatagtttgcagtgatagaaacaggtttcaaaactcagtcaactcgaccg 8520
QY 8521 TTTGATACATCTCAGACACCACCTACATTCAGTAGTTTAGTCCCTAGATTAATAATACAGAA 8580
Db 8521 ttgtatcatctcagacacacactacattcagtagtttagatgcctagaaataatagagaa 8580
QY 8581 GGAAGGAGATGGCTCTCTCTCTCTCATGTGTTTCTTCTGATGAGCTTGAATACACAT 8640
Db 8581 ggaagagatggctctctctctctctca ttggttctctctctgagtgagcttgaatcaat 8640
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Db 8641 gaagggaaacagcagaaaaacaacaaactgactcactcagctgctcatgtttctctttaaagtc 8700
QY 8701 CTTGAAAGGAAGTCTCTGGAATGTGACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8760
Db 8701 cctgaaaggaaggtcctggaaatgtgactcctctctctctctctctctctctctctctctct 8760
QY 8761 TTTCTTTGGACCTTACCAAGGACTGTAAATTGGTGGGACAGCTAGTGGCCCTCTCTGGGC 8820
Db 8761 ttcttttggaccctacgaaagactgaattggtgggacagctagtggccctgctggggc 8820
QY 8821 TTCACACACCGTGTCTCTCTAGCCAGTCCCTCTGAGTGCAGAACTCTCTGGTGGTATTTC 8880
Db 8821 ttcacacacggtgtcctcccttagggccagtgccctctgagtcagaaactcctgggtgatttc 8880
QY 8881 CCTCAATGAAGTGGAGTAAGCTCTCTCATTTTTCAGATGTTATTAATGGAAGCCACCAAGTG 8940
Db 8881 cctcaatgaagtgaggcaagct 8940
QY 8941 GCTTAGAGGATGCCAGGTCTCTTCATGAGCCACTGGGGTTCGGGTGTCACATTAATAAAA 9000
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QY 9001 AAAATCTAACCCAGGACATTCAGGAATTCCTAGATTCTGGGAAATCAGTTCCCATGTCAT 9060
Db 9001 aaaatctaaaccaggacattcaggaaattgctagattctgggaaatccagttcaccatgttca 9060
QY 9061 AAAGAGTCTTTTTTTTTTTTTTTTGTGAGACTTATTGCCCAGGCTGGAGTGCATGGCATGAT 9120
Db 9061 aaagagttcttt 9120
QY 9121 CTCGGCTCAGTGAACCTCTGCCCTCCAGGTTCAAGGATTTCTCTCTCTCAGCCCTCCCA 9180
Db 9121 ctccgctcaactgaacctctgcctcccaggttcaagcgattctctctctctcagcctccca 9180
QY 9181 AGTACCTGGGATTAACGGCTGACCCACCATGCCCCGCTAAATTTTGTATTTTGTAGTAGA 9240
Db 9181 agtagctgggaattacagagcgtgcaccacca tgcgccggcctaatttttttttttttttttttt 9240

[illegible]

QY	10321	CATTTTAAATCTTAAATCACCTCTGGCAAAACCATTCACAACAACCATGTAGTAAAGAGAA	10380
Db	10321	caatttaaatctctatccctctggcaaaaccattccaacaacctggtagtaagaagaa	10380
QY	10381	GGTGACACCTGGTGGCCATAGGTAATGTACACGGTGGTCCGGTGACACAGAGATGCAG	10440
Db	10381	gggtgacacctgggtggccataggtaaatgtaccacggtggccggtgaccagagatgcag	10440
QY	10441	CGCTGAGGGTTTCTGAAGGTAAAGGAATTAAGAAATGGGTGGAGGGCGGTGCACCTGGAA	10500
Db	10441	cgctgaggggtttcctggaagtgaaaggaataaagaatgggtggaggggctgacctggaa	10500
QY	10501	ATCACTTGTAGAAAAAGCCCTGAAAATTTTGAGAAAAACAAGAAACTACTTACCAG	10560
Db	10501	atcacttgtagagaaaagccctgaaaatttgagaaaaacaagaactacttaccag	10560
QY	10561	CTATTGTGAATTCAGGATCAGGCCATTCGTGAGTGCTGAACTGGGGAAACAACACAG	10620
Db	10561	ctatttgatctgtgaatcagcaagccattgtgagctgctgcactgggaaccaacacag	10620
QY	10621	AAGGAAAAACAACCACTCTGATAATCATTTAGTCAAGTACAGCAGGTGATTGAGGACTGC	10680
Db	10621	aaggaaaaacaaccactctgataatcattgagtcgaagtacagcagggtgattgaggaactgc	10680
QY	10681	TCAGAGGTACAGGCCAAAATCTTATGTTGTATTATTAATATGATCTTTATAATACTGT	10740
Db	10681	tgaggggtacaggccaaattctatgttggtattataataatgtcatcttataactgt	10740
QY	10741	CAGTATTTTATAAACATCTTCTCAAAACTCACACACATTTTAAAAACAAAACACTGCTC	10800
Db	10741	cagtattttaaaaaattcttcaaaactcacacacattcaaaaacaaaactgtctc	10800
QY	10801	TAAATCCCAAAATTTTTCATAAAC	10825
Db	10801	taaaatcccaaaatttttcataaac	10825

RESULT	4	
AAC68427		
ID	AAC68427	standard; DNA; 10825 BP.
XX		
AC	AAC68427;	
XX		
DT	21-FEB-2001	(first entry)
XX		
DE	Human hereditary hemochromatosis 24d2 mutation DNA.	
XX		
XX	HH; hereditary hemochromatosis; chelation agent;	
KW	T-cell differentiation factor; iron overload; ds.	
KW		
XX		
OS	Homo sapiens.	
XX		
XX	US6140305-A.	
PN		
XX		
PD	31-OCT-2000.	
XX		
EF	04-APR-1997;	97US-0834497.
XX		
PR	04-APR-1996;	96US-0630912.
XX		
PR	16-APR-1996;	96US-0632673.
PR	23-MAY-1996;	96US-0652265.
XX		
PA	(BIRA) BIO-RAD LAB INC.	
XX		
XX	Thomas WJ,	Drayna DT, Ruddy D, Tsuchi
PI	Feder JN;	
PI		
XX		
XX	WPI; 2001-006341/01.	
DR	P-PSDB; AAB36871.	
DR		
XX		
PT	New hereditary hemochromatosis gene products or pol	
PT	for treating hereditary hemochromatosis in a patien	
PT	chelation agent alleviating iron overload -	

QY 4141 GAATTTGCTTCTGAGATCATTTGGTCCTTGGGGATGGTGAAATAGGGACCTATTTCCTT 4200
DB 4141 gaatttgcttctgagatcatttggctcttgggtggtggaataggacctatttctt 4200
QY 4201 TGGTTGCAGTTTAAAGGCTGGGATTTTTCCAGAGTCCACACCCCTGCAGGTCATCCCTG 4260
DB 4201 tggttgcagtttaaaggctgggattttccagagtccacacccctgcaggctcactcg 4260
QY 4261 GCCTGTGAATGCAAGAACACAGTACGAGGGCTACTGGAAGTACGGGTATGATGGG 4320
DB 4261 gctgtgaatgcaagaaacacagtagcagggctactggaagtacgggtatgatggg 4320
QY 4321 CAGGACCACCTTGAATTTGCGCCCTGCACACTGGATTTGGAGAGCAGAACCCAGGGCC 4380
DB 4321 caggaccaccttgaatttgcgcctgcacactggattggagagcagaaaccagggcc 4380
QY 4381 TGGCCCCACCAAGCTGGAGTGGGAAGGCACAGATTCGGGCCAGGCAGAACAGGCCCTAC 4440
DB 4381 tggccccaagctggagtggaaagcacaagattcggccaggcagaacaggccctac 4440
QY 4441 CTGGAGAGGGACTCCCTGCACAGCTGCAGAGTGTCTGGAGCTGGGAGAGGTGTTTTG 4500
DB 4441 ctggagaggactccctgcacactgcagcagttgctggagctgggagaggtgtttg 4500
QY 4501 GACCAACAAGTATGGTGGAAACACACTTCTGCCCTTATCTCTAGTGGCAGAGTGGAGG 4560
DB 4501 gaccaacaagtatagggtggaaacacactctgccctatactctagtggcagagtggagg 4560
QY 4561 AGGTTGACGGGACAGGAATCCCTGGTGGAGTTTCACAGGTGGGTGAGGCTGTGGCTC 4620
DB 4561 aggttgaggggacaggaatccctggttcggagtttcagagtgggctgaggtgtgtgctc 4620
QY 4621 TCCAAATCTGGGAAGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTAGAGATGTA 4680
DB 4621 tccaaattctgggaaggactttctcaatcctagagttctacctataattgagatgta 4680
QY 4681 TGAGACGCCAACAGTCATGCGGTTTAAATTCCTTCTTCATGTCATATGCTCAAGGGAA 4740
DB 4681 tgagacagccaagtcagtgggtttaaatttcttctccatgcatggctcaaggaa 4740
QY 4741 GTGTCTATGGCCCTGTCTTTTATTAAACCAATAATCTTTGTATATTTATACCTGTAA 4800
DB 4741 gtgtctaaggccctgtcttttattaaaccaataattctttgtatattatcacctgttaa 4800
QY 4801 AAATTCAGAAATGTCAAGCCGGCAGCGTGGCTCACCCCTGTAAATCCCAGCACTTTGGG 4860
DB 4801 aaattcagaaatgtcaagccggcacgggtggtcacccctgtaatcccagcactttggg 4860
QY 4861 AGGCGGAGCGGGTGGTCACAAGGTCAGGAGTTTGACACCAAGCCTGACCAACATGGTGAA 4920
DB 4861 aggcggagcggggtggtcacaaggtcaggagtttgagaccagcctgaccacaatggtaa 4920
QY 4921 ACCGCTCTCTAAAAAATACAAAAATTAGCTGGTCACAGTCATGCGCACCTGTAGTCCCA 4980
DB 4921 accgctctctaaaaatacaaaaaattagctggccaagtcatgycacctgtagtccca 4980
QY 4981 GCTAATGGAAGGCTGAGGCGAGGATCGCTTGAACCTGGGAAGCGGAAGTTGCACTGA 5040
DB 4981 gctaattggaaggctgagcgaggagcagctgtgaacctgggaagcggaagtgcactga 5040
QY 5041 GCCAAGATCGGCCACTTATCCAGCTCAGGCTAGGCAGCAGAGTGACATTCATCTTAAAAA 5100
DB 5041 gccaaagtcgcgcactgcactccagcctaggcgagcagatgagactccatcttaaaaaa 5100
QY 5101 AAAAAAATAAAAAAGAGAAATTCAGAGATCTCAGGTATCATATGAATACCAAGGACAAA 5160
DB 5101 aaaaaaataaaaaagagaattcagaga cctcagctcatacatgaatcaccaggacaaa 5160
QY 5161 ATATCAAGTGGGCCACTTATCAGAGTAGAAGATCTCTTTAGGTTAAAGTTTCTTTTCAT 5220
DB 5161 atatcaagtggccacttatcagtagaagaatccttttaggttaaaagtttctttcat 5220

QY 5221 AGAACAATAGCAATAATATCAGCTGAAGCTACCTATCTTTACAGTCCGCTTCTTATACAAATGC 5280
DB 5221 agaacaatagaacaataaLcactgaagctacctacttacaagtcogcttcttataacaatgc 5280
QY 5281 CTCCTAGGTTGACCCAGGTGAAACTGACCATCTGTATTCAATCATTTTCAATGACACATAA 5340
DB 5281 ctctcaggctgacccagggtgaacctgacctctgcatcaatcacttccaatgacacataa 5340
QY 5341 AGGGCAATTTTATCTATCAGAAACAAGAACATGGGTAAACAGATATGTATATTTACATGTG 5400
DB 5341 agggcaattttatctatcatcagaacaagaacaLgggtaacagataLgtatatattacatgtg 5400
QY 5401 AGAGAACAAAGCTGATCTGACTGCTCTCAAGTGACACTGTGTTAGAGTCCAAATCTTAGG 5460
DB 5401 aggaagaaacagctgactgactgctctccaagtgcactgtgttagagtccaatcttagg 5460
QY 5461 ACACAAAATGGTGTCTCTCTGTAGCTTGTTTTCTGAAAAGGGTATTCTCTTCTCTCC 5520
DB 5461 acacaaaaLgggtgtctctctctgactgtgtttttctgaaaagggtatttcttcttctctcc 5520
QY 5521 AACCTATAGAAGAAAGTGAAGTCCAGTCTTCCTGGCAAGGGTAAACAGATCCCTCTCTC 5580
DB 5521 aacctatagaagaaagtgaagttccagctctccctggcagggttaaacagatccccctctc 5580
QY 5581 CTCATCTTCTCTTTCCTGTCAGAGTGCCTCTCTTGGTGAAGGTGACACATCATGTGACC 5640
DB 5581 ctcatcttctctcttctctgccaagtgcactcttgggtgaaggtgacacatcatgtgacc 5640
QY 5641 TCTTCAGTCACCACACTCTACGGGTGTGGGGCTTGAATCTACTACCTCCAGAACATCACCATTG 5700
DB 5641 tcttcagtgaccactctacggtgtctcgggcttgaactactaccctcccaagaacatccactg 5700
QY 5701 AAGTGGCTGAAGGATGAAGCAGCCAATGGATGCCAAGAGTTCGAACCTTAAAGACGTATTG 5760
DB 5701 aagtggctgaaggataagcagccaatLggatgcgaaggagttcgaacctaaagacgtattg 5760
QY 5761 CCCAATGGGGATGGGACCTACCAGGGCTGGATAAACCCTTGGCTGTACCCCTCGGGGAAGAG 5820
DB 5761 cccaaLggggaatgggaacctaccagggtcggataaacctLgggtgtaccctctggggaagag 5820
QY 5821 CAGAGATATACGTACCAAGTGGAGCCAGCCAGGCTGGATCGGATCAGCCCTCATTTGTGATCTGG 5880
DB 5821 cagagataLactgtccaggtggagcaaccagcggcctggatLcagccctcatgtgatctgg 5880
QY 5881 GGTATGTGACTGATGAGAGCCAGGAGCTGAGAAATCTATTGGGGGTTGAGAGGAGTGCC 5940
DB 5881 ggLtgtactgatgagccaggagctgagaaaaLctattgggggttgagagagtgcc 5940
QY 5941 TGAGGAGGTAAATTATGGCAGTGAGATGAGATCTGCTCTTTTGTAGGGGTGGGCTGAGG 6000
DB 5941 tgaggaggtaatttatggcagtgagataLgaggatactgctcttgttaggggggtgggtgagg 6000
QY 6001 GTGGCAATCAAGGCTTTAACTTGCTTTTCTGTTTTAGAGCCCTCACCGCTCGCACCC 6060
DB 6001 gtggcaatcaaggctttaactgtctttctgttttagagccctcacogtctggcaccc 6060
QY 6061 TAGTCATTTGGGTCATFCAGTGGAAATGTGTTTTGTCTCTCATCTTTTCATTGGAATTT 6120
DB 6061 tagtcattggagtcactcagtggaattgctgttttLgtcgtcatcttgttcatttggaattt 6120
QY 6121 TGTTCATATATTAAAGAAAGAGCGAGGTTCAAGTCAGTAGGAACAAGGGGCAAGCTCTCT 6180
DB 6121 tgttcataataattaaagaaagagcgagggttccaagtLgagttagaaacaagggggaatctct 6180
QY 6181 TAGTACTCTGCCCCAGGCACAGTGGGAAGGGGCAGAGGGGATCTGGCATCATATGGG 6240
DB 6181 tagtaacctctgccccagggcagatgggaaagggggcagaggggatactggcatccatggg 6240
QY 6241 AAGCATTTTCTCATTTATTTATTTCTTTGGGACACCCAGCAGCTCCCTGGGAGACAGAAAT 6300
DB 6241 aagcatttttctcatttatcttcttgggacaccagcagctccctgggagagacagaaat 6300
QY 6301 AATGGTCTCTCCCGAGAAATGAAGTCTCTAAATTCACAAACATCTTCAGAGCACCTACTAT 6360

Db 6301 aatggtctccccagaatgaaagtctctaatccaacaactcttcoagagcacctactat 6360
QY 6361 TTGTGCAAGAGCTGTTTAAGGTAGTACAGGGCTTTTGAGGTTGAGAGTCACGTGGCTAT 6420
Db 6361 ttgcaagagctgcttaaggttagtacagggctttgaggttgaagtcactgtggetat 6420
QY 6421 TCTCAGAACCCAAATCTGGTAGGGAATCAAAATGTATAGCAAGTAATATGACTTAAAGAAG 6480
Db 6421 tctcagaacccaaatctcgttagggaatgaattatgacgaagtaaatgtagttaaagaag 6480
QY 6481 ACCCATGAGGTCTTAAGCAGGAGCAAGCAAAATGCTTAGGGTGTCAAGGAAGAATG 6540
Db 6481 acccatgaggtcctaaagcgaggaagcaaatgcttaggtgtcaaaaggaagaatg 6540
QY 6541 ATCACAATTCAGCTGGGATCAAGATAGCCTTCTGGATCTTTGAAGAGAGCTGATTTCCA 6600
Db 6541 a tccacatcagctgggataagaatagcctctcgtgattcttgaggaagctggattcca 6600
QY 6601 TTAGGTGAGGTTGAAGATCATGGAGGTCTACACAGACGGAGCAACCATGCCAAGTAGGA 6660
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QY 6721 AGCTATCACTACCAATTAATGATCTTACCCCTGACACATCTGTGGTGTAGGGAAGA 6780
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QY 6901 AATGTTGTTTAAGAAAGTTAGATGAGAGGTGAGGAGACCGTTAGAAAGCCAAATAAGCAT 6960
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QY 6961 TTCCAGATGAGAGATAATGGTTCCTTGAATCCAATAGTCCCGAGTCTAAATTCAGATGG 7020
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QY 7021 GTGAATGAGGAATAAGGAACAGAGAGAGGCAAGATGGTGCCTAGTTTGTGATGCCT 7080
Db 7021 gtgaatgaggaataaaggaagagagaagaggaagatgg tgcctaggtttgtgatgct 7080
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QY 7141 TGAGTGACACGACGCTCAGACTCACTGTGGGAGGAGACAAAACCTAGAGACTCAAGA 7200
Db 7141 tgagtgacacgcgctcagactcaactgtgggaaggagacaaaactlagactcaaga 7200
QY 7201 GGGAGTGATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTTAACATAGAATTT 7260
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QY 7261 GCCTCAGCAACTCCTTGATTTTAGCCTTCTGTTCATTTCCTCAAAAGATTTCCCCAT 7320
Db 7261 gcttcagcaactccttgatttagcctctctgttca cttcctcaaaagatttccccat 7320
QY 7321 TTAGGTTTCTCAGTTCCGCATGCGGTGATCCCTAGCTGTGACTCTCCCTCGAACTG 7380
Db 7321 ttaggtttctgagttcctgcgctgcgg tga cccctagctgtgacctctccccggaaactg 7380
QY 7381 TCTCTCATGACCTCAAGCTGCATCTAGAGGCTTCCCTTCATTTCCTCGCTCACCTCAGAG 7440
Db 7381 tctctcatgacctcaagctgcatactagaggttctctcattcttcctccgtcacctcagag 7440

Db 7381 tctctcatgaaacctcaagctgcatactagaggttctctcattcttcctccgtcacctcagag 7440
QY 7441 ACATACACCTATCTCATTTTCATTTCCTATTTTTGGAGAGGACTCCTTAAATTTGGGGA 7500
Db 7441 acatacacctatctcatcttctcatttcttatttttggaaagagactccttaatttggggga 7500
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Db 7501 cttacatgattctatctttaaaca cctgagaaaaagctttgaacctggagacgttggctagccat 7560
QY 7561 AACCTTACCAGATTTTACACATGTATCTATGCAATTTCTGGACCCGTTCAACTTTTCTCT 7620
Db 7561 aaccttaccagatcttttacacatgtatcatgcatttctggaccogttcaacttttctct 7620
QY 7621 TTGAATCCTCTCTCTGTGTGTACCCAGTAATCTATCTGTCACCAAGCCTTTGGGGATTTCTTC 7680
Db 7621 ttgaatcctctctctgtgtttaccacaglaactcatcctgcaccaagccttggggattctctc 7680
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Db 7681 catctgattgtgagtgagttgcacagctatgaagcgtgtacactgcacgaatlgaaagag 7740
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QY 7861 AGTGTGATACAGATTTCGAAAGCTTTAATGGTGCCTTCATTTTGGGATGTACTCTAGTAT 7920
Db 7861 aggtgtcatacagatttgcgaagttaaagggtgccttcatttggagtgactctagtat 7920
QY 7921 TCAGAGCTGAAGAAACACAAATTTTCTACCTGTGTCTCTCTCTGTTCTGATGATAATGAAA 7980
Db 7921 tccagacctgaagaatcaacaataatttctacctggtctctcctgttctgtataatgaaa 7980
QY 7981 ATTATGATAGGATGATAAAGCACATTACTGTGTGCCACTCTTCTGAGCACCTACTTAA 8040
Db 7981 attatgaataaggatgataaaaagcacttactctgtgtccagctctctgtgagcacctactta 8040
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Db 8041 catgcattactgcagtcactcttcaataattctatgataagtagtactattatcccat 8100
QY 8101 TTTCTTTTAAATGAGAAAGTGAAGTAGGCCGGGACGGTGCTCACGCCGTGTAATCCC 8160
Db 8101 ttcttttttaaatgaagaaagtgaagtggcggggcacggtggtcacgcctgtaatccc 8160
QY 8161 AGCAGTTTGGGAGGCCAAAGCGGTGGATCACAGGCTCAGGAGATCGAGCCATCTCTGCC 8220
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QY 8221 TAACATGGTGAAACCCCATCTCTTAATAAAAAATACAAAAATTTAGCTGGCGCTGGTGGCAG 8280
Db 8221 taacatggtgaaaccccatctctaa taaaaatacaaaaaatagctggcggtgtggcag 8280
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QY 8341 CAGAGCTTGAGTGAGCCGAGTTTGGCCACTGCCTCAGCCTAGCTGACAGAGTGAGA 8400
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Db 8401 ctccatctcaaaaaataaaaaataaaaaataaaaaataaaaaataaaaaataaaaaata 8460
QY 8461 TAGAGTATCTCATGTTGTGCTAGTAGAACAAGGTTTCAAACTCAGTCAATCTGACCG 8520
Db 8461 tagagtatctcatagttgtcagtgatagaacagggttttcaaaactcagtcaactcagccg 8520

QY	2521	TATATCTGAAGAACTTCTCTGAAGATTTCTATGTTGTGTGAGAGAAGAAGATTTGG	2580
Db	2521		2580
QY	2521	taTattctgaagaaagtctgtgaagattcttatgttgtgtgagagaagaagaattgg	2580
Db	2521		2580
QY	2581	CTGGGTGTAGTAGCTCATGCCAAGCAGGAGGCCAAGAGAGACGATTCCTTGAGCTCAGGA	2640
Db	2581		2640
QY	2581	ctgggtgtagtagtcatgtccaagagagagccaaagagagacagattctctgagctcaggga	2640
Db	2581		2640
QY	2641	GTTCAAGACCGCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAAATACAAAAATTA	2700
Db	2641		2700
QY	2641	gttcaagaccagctgtggcagacacagacgaaacccctctctacaaaaatacaaaaatta	2700
Db	2641		2700
QY	2701	GCTGGGTGTGTGGCATGCACCTGTGATCCTAGCTACTTCGGGAGGCTGAGGTGGAGGTA	2760
Db	2701		2760
QY	2701	gcitgggtgtgtgtgcatgacctgttgatcctagtactctgggaagcttgaagtsgagggta	2760
Db	2701		2760
QY	2761	TTGCTTTGAGCCACGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCACATGTTACTTTCAGC	2820
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QY	2761	ttgctttgagccaggaagtgtgaggtgcagtgagccatgactgtgcacgtgtacttcagc	2820
Db	2761		2820
QY	2821	CTAGGTGCACAGCAAGACCCCTGTCCCTCTGACCCCTGAAAAAGAGAAGATTAAAGT	2880
Db	2821		2880
QY	2821	ctaggtgcagagcaagacctgtctcccttgacccctgaaaagagagaagattaaagt	2880
Db	2821		2880
QY	2881	TGACTTTGTCTTTATTTTAAATTTTATTGGCTTGAGCAGTGGGGTAATTTGGCAATGCCAT	2940
Db	2881		2940
QY	2881	tgactttgtctcttattttaattttatttggctgagcagtggggttaatttggcaatgcca	2940
Db	2881		2940
QY	2941	TTCTGAGATGGTCAAGCGCAGAGAAAGACGAGTTTGGGGTAAATCAAGGATCTGCATTTG	3000
Db	2941		3000
QY	2941	tcttgagatgtgtgaagggcagagaaagagcagtttctggggttaaaatcaagggatcttgcatttg	3000
Db	2941		3000
QY	3001	GGACATGTTTAAGTTTGAGATTCCAGTCAGGCTTCCAGTGTGTGAGGCCACATAGGCAGTT	3060
Db	3001		3060
QY	3001	ggacatgtttaagtttgagatttcagtcaggttccaaagtggtgagggccacataggcagtt	3060
Db	3001		3060
QY	3061	CAGTGTAAAGATTCAGSGACCAAGGCTGGSGCAGGTTGCTCACTTCTGTAATCCCGACCT	3120
Db	3061		3120
QY	3061	cagtgtaaagatctcagggaccaaggtctgggacagcttgcctcacttctgttaatccccagcact	3120
Db	3061		3120
QY	3121	TTGGTGGCTGAGGCAGGTAGATCATTTGAGGTGAGGAGTTTGACACAAGCTTGCCCAACA	3180
Db	3121		3180
QY	3121	ttggtggctgaggcaggtagatcatttgaggtcgaggaagtttgagacaagcttggccaaca	3180
Db	3121		3180
QY	3181	TGTTGAACCCCATGCTACTATAAATACAAAAATTACCTTGGTGTGGTGGCGCACGCTT	3240
Db	3181		3240
QY	3181	tggtgaaaccccatgctactataaaatacaaaaaatgacctggctgtgtgtgtggcagcgcct	3240
Db	3181		3240
QY	3241	ATAGTCCCGAGTTTTCAGGAGGCTTAGTTAGTAGAATCCCTTTGAACCCAGGAGGTGCAGG	3300
Db	3241		3300
QY	3241	atagtccaggttttcaggaggttaggttaggaagatcccttgaacccaggaggtgcagg	3300
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QY	3301	TTGCAGTGAGCTGAGATTGCGCATCTGCACCTCCAGCTGGGTGATAGAGTGAGACTCTGT	3360
Db	3301		3360
QY	3301	ttgcagtgaagctgagattgtgcactgtcactccagctcgggtgtagtagtgagactctgt	3360
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QY	3361	CTCAAAAAAFAAAAAAFAAAAAAFAAAAAAFAAAAAAFAAAAAAFAAAAAAFAAAAAA	3420
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QY	3361	ctcaaaaaaafaaaaaafaaaaaafaaaaaafaaaaaafaaaaaafaaaaaafaaaaaaf	3420
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QY	3421	TCTAATTTGCCCTTGACCACTCCTGAGTTCACTACCATGGCTGAGACACACCTTTAAC	3480
Db	3421		3480
QY	3421	tctaatttgcccttgagaccaactcctgatttcaactacatggctgtagacacaccttaac	3480
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QY	3481	ATTTTCTTAGAATCCACAGCTTTAGTTGGAGTCTGTCTAATCATGAGTATTTGGAATAGGAT	3540
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QY	3481	attttctagaatccacagcttttagtgagctgtgtctaactcatgagtatctggaataggat	3540
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QY	3541	CTGGGGCAGTGAGGGGTGGGCGCCACGTGTGGCAGAGAAAACCAACAAAGGAAGAGC	3600
Db	3541		3600
QY	3541	ctgggggcagtgaggggggtggcagccaagtgtggcagagaaaagcacacaaggaagagc	3600
Db	3541		3600

Qy	3601	ACCAGACGCTGTCATATGGAGAAAGACAGAGACTGCAACTCACCCCTTCACAAAATGAGGA	3660
Db	3601	accagacgtgcatatgaaagaagacagagactgcaactcacccctcacaaaatgagga	3660
Qy	3661	CCAGACAGCTGATGATGAGTTGATGCAGAGTGTTGGAGCCCTCAACATCTCTGCTCCC	3720
Db	3661	ccagacagctgatggtatgagtgatgcaggtgtgtagcctcaacatcctgctccc	3720
Qy	3721	CTCCTACTACATATGGTTAAGGCGTGTTCCTCTGTCTCCAGGTTACACTCTCTGCACTA	3780
Db	3721	ctcctaatacaatggttaagggctgtgctctgtgctccaggttcacactctcgcacta	3780
Qy	3781	QCTCTTCATGGTGCCTTCAGACAGACACCTGGTCTCTTCCCTTGTGTGAAGCTTTGGGCTA	3840
Db	3781	cctctcatgggtgctccagagcaggaaccttggtcttctctgttgaagcttgggcta	3840
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Qy	3901	TCCATGGGTTTCCAGTAGAAATTTCAAGCCAGATGTGGCTGCAGCTCAGACTCTGAA	3960
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Qy	4021	CAAGGGTATGTGAGAGGGGGCCTACCTTCTCCTGAGTGTGCAGAGCTTTTCATCTTTTC	4080
Db	4021	caaaggctatgtggagaggggcccacctcctcctgaggttgctcagagcttttcattcttc	4080
Qy	4081	ATGCATCTTCAAGGAAACAGCTGGAAGCTGAGGCTGTGGAGCAGGGAGAGGAGAG	4140
Db	4081	atgcatacttgaaggaaacacgttggaagctctgaggtctgtggagacagggagaggaag	4140
Qy	4141	GAATTTGCTTCCTGAGATCATTTGGTCTTGGGGATPGTGGAAATAGGGAOCTATTCCTT	4200
Db	4141	gaatttcttctcgtagatcatatttggctctggga tgg tggaaataggagacattctctt	4200
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Qy	4321	CAGCACACCTTGAAATTCCTGCCCTGCACACTTGGATTGGAGACAGCAAGACCCAGGGCC	4380
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Qy	4381	TGGGCCCAAGCTGGAGTGGGAAGGCACAGATTCGGGGCCAGCAGACAGGGCCTAC	4440
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Qy	4561	AGGTTGACAGGGCAGGAATCCCTGGTTGGAGTTTCAGAGTGGCTGGGCTGTGTGCCCTC	4620
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Qy	4621	TCCAAATCTGGGAGGGGACTTTCATATCCCTAGAGTCTCTACCTATATATTTGAGATGTA	4680
Db	4621	tccaaattctgggaaggagacttctcaatctctagagctctcaacctataaattgagatgta	4680
Qy	4681	TGAGACAGCCACAAGTCAVGGGTTTAAATTTCTTTTCTCCATGCATATGGCTCAAAAGGAA	4740

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[illegible]

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Qy	10201	gTTAAATTTTTTAAATAGAAATTTTAAAGTCCTCATTTCTTTTCGGTGTTTTTTTAAAGCTTAA	10260
Db	10201	gttaattttttaaataagaaatttaagtcctcatttcttcttogggtgttttttaagcttaa	10260
Qy	10261	TTTTTCTGGCTTTATTCATAAATCTTTAAGTGCAACTACATTTTGAAANAATCAAGACCTG	10320
Db	10261	ttttctggcttatttcataaattcttaagtcacactacatttgaaataatcaaaagacctg	10320
Qy	10321	CATTTTAAATTTCTTATTCACCTCTGGCAAAAACCATTCACAAACCATGGTAGTAAAGAGAA	10380
Db	10321	cattttaaatcttattccctctgcaaaaccttcacaaaccactggtagtaaaagagaa	10380
Qy	10381	GGGTGACACTGGTGGCCATAGTAAATGTACACGGTGTGCGGTGACACAGATGCGAG	10440
Db	10381	gggtgacactggtggccataggtaaattgaccacggtggtccggtagccagagatgcag	10440
Qy	10441	CGCTGAGGGTTTTCTCTGAAGGTAAAGGAATAAACAATGGGTGGAGGGCGTGCACCTGGAA	10500
Db	10441	cgcctgaggggtttctctgaaaggcaagggaataaagaaatgggtgagggggcgtgcactcgaa	10500
Qy	10501	ATCACCTGTAGAGAAAGCCCTCGAAAATTTTGAGAAAACAACAAGAAACTACTTTACCAG	10560
Db	10501	atcactttagagaaaagccctgaaaatttgagaaaacaaacaagaaactactttaccag	10560
Qy	10561	CTATTTGAATTCCTGGAATCACAGGCCAATTCCTGAGCTGCCTGAACCTGGGAACACAAACAG	10620
Db	10561	ctatttgaattgctcg9gaaatcacaggccattgctgagctgctgaaactg9gaaacacaaacag	10620
Qy	10621	AAGGAAAACAACCACTCTGTAATTAATTCATTGAGTCAAGTACAGCAGGTGATGTAGGACTGC	10680
Db	10621	aaggaaaacaaacactctgataactcatttgatgacgtcaagtcacagcaggtgattgaggactgc	10680
Qy	10681	TGAGAGGTACAGGCCAAAATCTTATGTGTATTATTAATATGTCATCTTATAATACTCTG	10740
Db	10681	tgagaggtacagggccaaaattcttattgtgtattataataatgtaactataataactgt	10740
Qy	10741	CAGTATTTTATAAACAATCTTTCACAAAACCTCACACATTTTAAANAACAACACTGCTCTC	10800
Db	10741	cagtattttataaaacattcttcacaaactcacacattttaaanaacaaacactgtctc	10800
Qy	10801	TAAATCCCGCAATTTTTCATPAAC	10825
Db	10801	taaaatccccaaatttttcoataaac	10825
RESULT 6			
AA96794			
ID	AA96794 standard; cDNA; 12146 BP.		
XX			
AC	AA96794;		
XX			
DT	19-FEB-2001 (first entry)		
XX			
DE	Genomic DNA of a histocompatibility iron loading (HFE) gene.		
XX			
KW	Human; histocompatibility iron loading protein; HFE protein;		
KW	major histocompatibility complex; non-classical class I gene;		
KW	chromosome 6p; iron disorder; haemochromatosis; ss.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	exon	1028..1324	
FT		/*tag= a	
FT		/number= 1	
FT	intron	1325..4651	
FT		/*tag= b	
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FT	exon	4652..4915	
FT		/*tag= c	
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FT intron 4916..5124
FT /*tag= d
FT /number= 2
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FT 10206..10637
FT /*tag= m

PN W0200058515-A1..

XX 05-OCT-2000.

PF 24-MAR-2000; 2000WO-US07982.

XX 26-MAR-1999; 99US-0277457.

XX (BILL-) BILLUPS-ROTHENBERG INC.

XX Rothenberg BE, Sawada-Hirai R, Barton JC;

XX WPI; 2000-647244/62.

XX Diagnosing an iron disorder e.g. hemochromatosis or a genetic
PT susceptibility to develop it, by determining the presence of a mutation
PT in exon 2 or an intron of a histocompatibility iron loading nucleic
PT acid -

PS Example 1; Page 21-28; 55pp; English.

XX The present sequence represents the human histocompatibility iron
CC loading (HFE) gene. The HFE gene is a major histocompatibility (MHC)
CC non-classical class I gene located on chromosome 6p. Mutations in the
CC gene lead to iron disorders. The specification describes a method for
CC diagnosing an iron disorder or a genetic susceptibility to develop the
CC disorder in a mammal. The method comprises determining the presence of
CC a mutation in exon 2 or an intron of a HFE gene or protein. The mutation
CC is not a C to G missense mutation at nucleotide 187 of the sequence
CC given in A96769 (Genbank Accession number U60319). The presence of the
CC mutation indicates the disorder or the genetic susceptibility to the
CC disorder. The method is used to diagnose an iron disorder
CC e.g. haemochromatosis, or a genetic susceptibility to develop it.

XX Sequence 12146 BP; 3383 A; 2474 C; 2911 G; 3378 T; 0 other;

Query Match 99.4%; Score 10760.2; DB 21; Length 12146;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 10813; Conservative 0; Mismatches 8; Indels 8; Gaps 4;

Qy 1 TCTAAGGTGAGATAAAATTTTAAATGTATGATTGAATTTTGAATATCATATAATTTA 60
|||||

Db 889 tctaaggttgagataaaaaatttttaaatgtatgattgaatttttgaaatacataaatatta 948
Qy 61 AATATCTAAAGTTTCAGATCAGAACATTCGGAAGCTACTTTCCCAATCAACAACACCCCT 120
|||||
Db 949 aatatctaaagtttcagatcagaacatttggaagctactttccccaatacaaacacccct 1008
Qy 121 TCAGGATTTAAAAACCAAGGGGACACTGTGATCACCTAGTGTGTTTCACAGAGGTACCTT 180
|||||
Db 1009 tcaggatttaaaacccaaggggacactggtacacctagttacacagcaggtacctt 1068
Qy 181 CTGCTGTAGGAGAGAGAGAACTAAAGTTCTGAAAGACCTGTGCTTTTCCACAGGAAGTT 240
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Db 1069 ctgctgtaggagagagagaactaaagttctgaaaagacctgtgtctttccacaggaagtt 1128
Qy 241 TTACTGGGCATCTCCTCAGCCTAGGCAATAGCTGTAGGCTGACTTCTGGAGCATCCCG 300
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Db 1129 ttactgggcattctcctgagcctaggcaatagctgtaggtgacttctgagccatccccg 1188
Qy 301 TTTCCCGCCGCCCAAGAGCGGAGATTAAACGGGGAGCTGCGGCCAGAGCTGGGGAA 360
|||||
Db 1189 ttccccgcccccaaaagcgagatttaacgggggacgtgagccagagctggggaa 1248
Qy 361 ATGGGCCCGGAGCCAGCGGCGCTTCTCCTCTCATGCTTTTTCAGACACCGCGGTCTTG 420
|||||
Db 1249 atgggccccgagccagggccggcgtctcctcctgatgtcttttgagaccggtctctg 1308
Qy 421 CAGGGCGCTTGTGCTGAGTCCGAGGGTGGCGGCGAACTAGGGCGCGCGGGGGTG 480
|||||
Db 1309 caggggcgcttgcgtgagtcgagggctcgggcggaactagggggcgggggggcg 1368
Qy 481 GAAAAATCGAACTAGCTTTTCTTGGCTTGGGAGTTTGCTAACTTTGGAGGACCTGC 540
|||||
Db 1369 gaaaaatcgaaactagcttttcttgcgttgggagtttgccttaactttggaggacctgc 1428
Qy 541 TCAACCTTATCCGCAAGCCCTCTCCTCTACTTTCTGCGTTCAGACCCCGCTGGAGGAGTC 600
|||||
Db 1429 tcaacccaatccgcaagccccctcctcctacttctctgctgccccagcccgctgaggagtgc 1488
Qy 601 CTACCACTGAACATGCAGATAGGGGTCCCTCGCCCGCAGGACCTGCCCCCTCCCGGCTGT 660
|||||
Db 1489 ctaccactgaactgcagataggggttcctcgcgccccagacctgccccctcccccgctgt 1548
Qy 661 CCGGGCTCTGGGAGTGACTTTTGGAAACCGCCACTCCCTCCCACTGCTGCTGCTGCTTT 720
|||||
Db 1549 cccggctctgcggagtgcacttttggaaacgccccactcccttcccccaactagaatgcttt 1608
Qy 721 TAAATAAATCTCGTACTTCTCTACTTGAGCTAGCTTAAGCCTGGGGCTCTTGAACCTGG 780
|||||
Db 1609 taaataaaatctcgtagcttccctcactgagctgagctaaagcctggggccttgaaccttg 1668
Qy 781 AACTCGGGTTTATTTCCAAATGTGCTGTCAGTGTGCTGCTTTTTCCTCCAGTCACTCCAAACAGG 840
|||||
Db 1669 aactcgggtttatttccaatgcagctgagagtttttccccagtcactctcccaaacagg 1728
Qy 841 AGTTCTTCCCTGAGTCTGCTGCGAGAGGCTGAGCAAAACCCACAGCAGGATCCGCACGG 900
|||||
Db 1729 aagtttccctgagtgcttgcggaagagctgagcaaacccacacagcagatcccgcaagg 1788
Qy 901 GGTTCCTCCTCAGAACGAATGCTTGGCGGCTGGGGCGCGCAAGAGTGGCGTGGGGA 960
|||||
Db 1789 ggtttccacctcagaaacgaatgctgtggcggtggggcgcaaaagagtggtggttgggga 1848
Qy 961 TCTGAATTTCTCACCATTCCACCCACTTTTGGTGAGACCTGGGGTGGAGGTCTCTAGAGGT 1020
|||||
Db 1849 tctgaattcttcaaccattccaccttttggtagacctgggggtggaggtctcttagggt 1908
Qy 1021 GGGAGGCTCCTGAGAGAGCGCCTACCTCGGGCCTTTCCCGACCTTTTGGCAATTTGTTT 1080
|||||
Db 1909 gggaggtcctgagagagggcctacctcgggcctttccccactcttggcaattgttctttt 1968
Qy 1081 GCCTGGAATAAATAGTATATGTAGTTTGAACGTTTGAACGTTTGAACGTAACAATTTCTTTTCGG 1140
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Db 1969 gctggaaaaattaaagtatatgttagttttgaacgttttagaactgaacaattctcttttogg 2028
|||||

QY	1141	CTAGGCTTTATTGATTTGCAATGTGCTGTAATTAAGAGGCCCTCTCTACAAAGTACTGA	1200	QY	2221	AATAAACAGTAGTCTCTGGGAGTAGAGCCAAAGAGTAGCTAATGGCTCAGAAAGAGGA	2280
Db	2029	ctaggctttattgatctgaatgtgctgtgtaataatgaaggccctctctacaaagtactga	2088	Db	3108	aataaacaaglagtgctggtggagtagagggccaagaagtagttaatgggctcagaagagga	3167
QY	1201	TAATGAACATGTAAAGCAATGCATCACTACTTAAGTTACATTTCAATCTGATCTTAATTTGA	1260	QY	2281	GCCACAAACAGGTTGTGCAGCGCCTGTAGGCTGTGGTGTGAATTTCTAGCAAGGAGTA	2340
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QY	1261	TTTTCACTAGGCATAGGAGGTAGGAGCTAATAATACGTTTATTTTACTAGAGTTAACT	1320	QY	2341	ACAGTGTACTGTACAGGCTTTTAAAGATTGCTCTGGCTGTATGTGAAAGCAGAAATG	2400
Db	2149	ttttcactagcataggaggttagagctaatataacgtttattttactagaagttaact	2208	Db	3228	acagtgaatctgtcacaggcttttaaaagatlgctctggtcgtctatgtggaagcagaatg	3287
QY	1321	GGAATTCAGATTATATAACTCCTTTTACAGTTTCAAAAGAACATAAATCTGTTTCTCG	1380	QY	2401	AAGGAGCAACAGTAAAAACAGGGAGCCAGCCAGGAAGCTGTTACACAGTCCAGGCAAG	2460
Db	2209	ggaattcagattataaactctttcaggttacaagaacataataactcgtgtttctcg	2268	Db	3288	aaggaggcaacagtaaaagcaggagccagcaggaagctgttacacagtcaggccaag	3347
QY	1381	ATGTTATTTCAAGTACAGCTGCTCTCTAATCTTACTTACAGAGTGAATTTGCCCTGTAG	1440	QY	2461	AGGTAGTGGAGTGGCTGGTGGGAACACAGAAAGGAGTGACAAACCATTGCTCCTGAA	2520
Db	2269	atgtatttcaagtactacagctgcttctaactcttagttgacagtgattttggccctgtag	2328	Db	3348	aggtagtgagtggtggtgggtgggtgggtgggtgggtgggtgggtgggtgggtgggtgaa	3407
QY	1441	TGTAGCACAGTGTCTGTGGGTACACGCCGCTCTAGACACAGCACCTTTGAGTTTGGTA	1500	QY	2521	TATATTTGAAGGAAGTTGCTGAAGGATTCTATGTTGTGTGAGAGAAAGAGAAATTTGG	2580
Db	2329	tgtagcacagtgctctggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt	2388	Db	3408	tatatctgaaggaagtgtgtgaagattctatgttgtgtagagaaagagaagaattgg	3467
QY	1501	CTAGCTGTATCCACATTTTACATGACAAAGATGAGGCATGGCACGGCTGCTTCTCTGG	1560	QY	2581	CTGGGTGTAGTAGCTCATGCCCAGAGGAGGCCAAGGAGAGCAGATTTCTTGAGCTCAGA	2640
Db	2389	ctacgtgtatccacattttcacatgacaaagatgaggaatgaggaatgaggaatgaggaatg	2448	Db	3468	ctgggtgttagtagctcatgccaaggagggagggccaaggagagagagagagagagagag	3527
QY	1561	CAAAATTTTCAATGTGTACACTGGGCTTTGGTGGCAGAGCTCATGCTCCACATTCATAGC	1620	QY	2641	GTTCAAGACACGCTGGGCAACACACAGCAAAACCCCTCTCTACAAAAATACAAAAATTA	2700
Db	2449	caaatatttcaatggttacacgggctgtgtggtggtggtggtggtggtggtggtggtggtg	2508	Db	3528	gttcaagaccagccttgggccaacacacagcaaaacccctctctacaaaaatacaaaaaat	3587
QY	1621	TATGATTTTAAACATCACACTGATTTAGAGTTGGAATATAAATTTATGTTGAGCAG	1680	QY	2701	GCTGGTGTGGTGGCATGCACCTGTGATCTTACTTACTCGGAGGCTGAGGTGGAGGTA	2760
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QY	1681	AAATATTATTGTTTACAAGTGTAAATGAGTCCAGCCATGTGTGACATGTTTCAAGCCC	1740	QY	2761	TTGCTTGACCCAGGAAAGTTGAGGCTGCAGTGCAGCCATGACTGTGCCACTGTACTCTAGC	2820
Db	2569	aaatattcattgtttacaagtgtaaatgagtcacagcagctgtgtgcactgtttcaagccc	2628	Db	3648	ttgcttgagcccaagagttgaggtgcagtgagccatgactgtgccactgtacttcagc	3707
QY	1741	CAAGGAGAGAGAGGGAACAAAGCTCTTACCCTTTGATATTTTGCATTTACTGGGAGA	1800	QY	2821	CTAGGTGACAGAGCAAGCCCTGTCTCCCTGACCCCTGMAAAAGAGAAAGATTTAAAGT	2880
Db	2629	caaaggagagagcgggaaacaagctcttaccctctgtatatttgcattctagtggagga	2688	Db	3708	ctaggtgacagagcaagaccctgtctccctgacccctgaaacagagagagagttaaagt	3767
QY	1801	GATGACATAAGCAAAATGACAGAAAGATATACAACTACAGGAATCATGGGTGTTGTA	1860	QY	2881	TGACTTGTGTTTATTTTATTTTATTTGCTGAGCTGAGCTGGGGTAAATTTGGCAATGCCAT	2940
Db	2689	gatgacaataagcaaatgagcagaaagatatatacaacatcaggaaatcatggtgtgtga	2748	Db	3768	tgacttgttcttatttatttatttatttatttatttatttatttatttatttatttatttattt	3827
QY	1861	GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGGTGCACATTTGAGCAGACATGAAGGA	1920	QY	2941	TTCTGAGATGGTGAAGGCAGAGAGAGACAGTCTTGGGTAAATCAAGCATCTGCATTTG	3000
Db	2749	gaagcagagaagtcaggccaagtcaactctgggctgacacttgagcagagacatgaagga	2808	Db	3828	ttctgaga tgggtgagggcagaggaagagcagcttggggtaaatcaaggatctgcattt-	3886
QY	1921	AATGAATATATTGACTGGGACAGTATTTCCAGGCAACATGAGTGGGCTGGCAAG	1980	QY	3001	GGACATGTTAAGTTTGAGATTTCCAGTTCAGGCTTCCAAGTGGTGAGGCCACATPAGCAGTT	3060
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QY	1981	TTGGAATAAAAGCGGTTTCTCAGCACACTACTCATGTGTGTGTGTGTGTGTGTGTGTGT	2040	QY	3061	CAGTGTAAAGATTCAGGACCAAGGCTGGCAGCGGTGCACCTTCTGTAATCCCAGCACT	3120
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QY	2101	CCTCCTACTACTAGTGTCTAGGAGCACTCCCCAGTCTTTGACAAACAAAAATGTCTCT	2160	QY	3181	TGTTGAAACCCCATNGTCTACTTAAATATACAAAATTTAGGCTGGTGTGGGGCGCAGCT	3240
Db	2988	cctccctactcactaggtgtcagagcaactccccagctcttgacaaccaaaaaatgtctct	3047	Db	4067	tggtgaaaccccatgtctactaaaaatacaaaaaattagcgtgtgtgtgtgtgtgtgtgtgt	4126
QY	2161	AAACTTTGCCACATGTCACTACCTAGTAGACAAACTCCTGGTTAAGAGCTCGGTTGAAAAA	2220	QY	3241	ATAGTCCCAGGTTTTCAGGAGGCTTAGGTAGGAGAAATCCCTTGAAACCCAGGAGGTGCAGG	3300
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				QY	3301	TTGCACTGAGCTGAGATTGTGCCACTCCGACTCCGAGCTGGGTGATAGAGTGAAGTCTGT	3360

Db 8565 ctccatctgattgattgagttgacagctatgaggtgtacactgcacgaatgga 8624
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Db 9525 acatgaagggaagcagcagaaaaacaaactgactcctcagctgtcatgttttctttaa 9584
QY 8697 AGTCCCTGAAGGAAGGTCCCTGGAATGACATCCCTTGTCTCTCTCTCTCTCTCTCTCT 8756
Db 9585 agtccctgaagggaaggtctggaatgtgactcccttgcctcctctgtctctctcttggca 9644
QY 8757 TTTCAATTTCTTTGGACCTTACGCAAGGACTGTAATTTGGTGGGACAGCTAGTGGCCCTGCT 8816

Db 9645 ttcatatttttggaccctacgcaaggactgtaattggtggggacagctagtgccctgct 9704
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QY 8877 TTTCCCTCAATGAAGTGGAGTAAAGTCTCTCAATTTTGAGATGTATTAATGAAGCACCA 8936
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Db 9825 agtggcttagaggatgcccaggtcttccatggagccactgggggttccgggtgcacattaa 9884
QY 8937 AAAAAAATCTAACAGAGACATTCAGGAATGTAGATTCTGGGAATCAGTTTCACCATG 9056
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Db 10125 tagagacagggttttcaacatgttggccaggtgggtctcgaactctctcagacctctgac 10184
QY 9237 CGCTGCTCGCCCTCCAAAGTCTGAGATTACAGGTGTGAGCCACCCCTGCCCCAGCCGT 9356
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QY 9357 CAAGAAGCTCTTAATATATATATATCCAGATGGCATGCTGTTTACTTTATGTTACTACATGCA 9416
Db 10245 caaagagctcttaataataataatccagatggcatgttttcttcttcttcttcttcttct 10304
QY 9417 CTGTGCTGCATAAATGTGTGTAACAGCATTTCTGCTTCAAGGGCAGGTGCTTCAGGATACC 9476
Db 10305 cttggctgcalaataatggttacaagcattctgtctgaaggcaggtgtctcagatacc 10364
QY 9477 ATATACAGCTCAGAAGTTCTCTCTTTAGGCATTAATAATTTAGCAAGATATCTCATCTCT 9536
Db 10365 atatacagctcagaagttctcttctttaggcattaaatttttagcaagatactctctct 10424
QY 9537 TCTTTTAAACCATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 9596
Db 10425 tctttaaaccattctctcttcttcttcttcttcttcttcttcttcttcttcttcttct 10484
QY 9597 ATTTACGCTCATTTGTAGAAAAAGCTATAAAATGAATACAAATTAAGCTGTTTATTAATAG 9656
Db 10485 atttacgctcatgtgaaaaagctataaaaatgaatacaattaaagctgttatttaattag 10544
QY 9657 CCAGTGAATAACTATTACAACTTGTCTATTACCTGTTAGTATTATTGTTGGCATTTAAAA 9716
Db 10545 ccagtgaaaaacttaacaaactgtctattacctgttagtattattgttgcattaaaaa 10604
QY 9717 TGCATATACTTTTAAATGATATTTGTTATTTGTTATCTGATGATTTTATTTGAAGTCTCT 9776
Db 10605 tgcataactttaataaagtgaactgtattgtatactgcagtatttattgaattctt 10664
QY 9777 GTTCATCTGTTGTATATACTTAAATCGCTTTGTCAATTTTGGAGACATTTATTTGCTCTCA 9836
Db 10665 gtctactgtgtatacttaacttaactcgtcttcttcttcttcttcttcttcttcttcttct 10724
QY 9837 ATTTCTTTTACATTTTGTCTTACGGAATATTTTCAATCACTGCTGGTACCGAATTAATCG 9896
Db 10725 atttctttacattttgtctctacggaattttcttcttcttcttcttcttcttcttcttct 10784

Qy	6777	AGAGAAATCAGAAAGAACGCCAGCTCATACAGAGTCCAAAGGGTCTTTTGGGATATTGGGTT	6836
Db	40325	AAAGAGAAATCAGAAAGAACGCCAGCTCATACAGAGTCCAAAGGGTCTTTTGGGAATATTGGGTT	40266
Qy	6837	ATGATCACATGGGGTGTCTAATTGAAGATCCCTAAGAAAGGAGGACACAGATCTCCCTTATAT	6896
Db	40265	ATGATCACATGGGGTGTCTAATTGAAGATCCCTAAGAAAGGAGGACACAGATCTCCCTTATAT	40206
Qy	6897	GGTGAATGTGTTTAAAGAAGTTAGATCGAGAGTGTAGGAGACACAGTTAGAAAGCCAAATAA	6956
Db	40205	GGTGAATGTGTTTAAAGAAGTTAGATCGAGAGTGTAGGAGACACAGTTAGAAAGCCAAATAA	40146
Qy	6957	GCATTTCCAGATGAGAGATAATGCTTCTGNAATCCAAATAGTCCCAAGCTCTAAATTCAG	7016
Db	40145	GCATTTCCAGATGAGAGATAATGCTTCTGNAATCCAAATAGTCCCAAGCTCTAAATTCAG	40086
Qy	7017	ATGGCTCAATAGGAGAAATAAAGGAAGAGAGAAAGCAAGATGGTGCCATAGTTTGTGAT	7076
Db	40085	ATGGGTGAATAGGAGAAATAAAGGAAGAGAGAAAGCAAGATGGTGCCATAGTTTGTGAT	40026
Qy	7077	GCCTCTTTCTCGGTCTCTTTGTCTCCACAGGAGAGCCATGGGGCACTACGTCTTTAGCTG	7136
Db	40025	GCCTCTTTCTCGGTCTCTTTGTCTCCACAGGAGAGCCATGGGGCACTACGTCTTTAGCTG	39966
Qy	7137	AACGTGAGTGCACACGACGCTGCAGACTCACTGTGGGAAGGAGACAAAACCTAGAGACTCA	7196
Db	39965	AACGTGAGTGCACACGAGCCGTCAGACTCACTGTGGGAAGGAGACAAAACCTAGAGACTCA	39906
Qy	7197	AAGAGGAGTGCATTTATGAGCTCTTCATGTCTCAGGAGAGAGTTGAACCTAAACATAGA	7256
Db	39905	AAGAGGAGTGCATTTATGAGCTCTTCATGTCTCAGGAGAGAGTTGAACCTAAACATAGA	39846
Qy	7257	AATTGCGCTGACGAACCTCCTTGATTTTACGCTTCNCGTTCATTTCCCTCAAAAGATTTCC	7316
Db	39845	AATTGCGCTGACGAACCTCCTTGATTTTACGCTTCNCGTTCATTTCCCTCAAAAGATTTCC	39786
Qy	7317	CCATTTAGGTTTCTGAGTTTCTGTGATCGCGGTGATCCCTAGCTGTGACCTCTCCCTCGGA	7376
Db	39785	CCATTTAGGTTTCTGAGTTTCTGTGATCGCGGTGATCCCTAGCTGTGACCTCTCCCTCGGA	39726
Qy	7377	ACTGTCTCTCATGAACCTCAACGTGCATCTAGAGGCTTCCTTCATTTCCCTCCGTCACTC	7436
Db	39725	ACTGTCTCTCATGAACCTCAACGTGCATCTAGAGGCTTCCTTCATTTCCCTCCGTCACTC	39666
Qy	7437	AGAGACATACACCTATGTTCATTTTCATTTCTTATTTTGGGAAGGAGGACTCCTTAAATTTGG	7496
Db	39665	AGAGACATACACCTATGTTCATTTTCATTTCTTATTTTGGGAAGGAGGACTCCTTAAATTTGG	39606
Qy	7497	GGGACTTACATGATTCATTTTAACTGAGAAAAGCTTTGAACCCCTGGGAGCTGGCTAG	7556
Db	39605	GGGACTTACATGATTCATTTTAACTGAGAAAAGCTTTGAACCCCTGGGAGCTGGCTAG	39546
Qy	7557	TCATAACCTTACCAGATTTTACACATGATCTATGATTTTCTTGGACCGTTCAACTTTT	7616
Db	39545	TCATAACCTTACCAGATTTTACACATGATCTATGATTTTCTTGGACCGTTCAACTTTT	39486
Qy	7617	TCCTTTGAATCCCTCTCTCTGTGTTTACCAGTAACATCATCTGTCCACCAAGCTTTGGGGATT	7676
Db	39485	TCCTTTGAATCCCTCTCTCTGTGTTTACCAGTAACATCATCTGTCCACCAAGCTTTGGGGATT	39426
Qy	7677	CTTCCATCTGATGTGATGTGAGTTTGCACAGCTATGAAGCTGTACACGTGCACGAATGGA	7736
Db	39425	CTTCCATCTGATGTGATGTGAGTTTGCACAGCTATGAAGCTGTACACGTGCACGAATGGA	39366
Qy	7737	AGAGGACCTGTCCCAAGAAAAAGCATATGCTATCTGTGGGTAGTATGATGGGTGTTTT	7796
Db	39365	AGAGGACCTGTCCCAAGAAAAAGCATATGCTATCTGTGGGTAGTATGATGGGTGTTTT	39306
Qy	7797	TACGAGGTAGGAGGCAAAATATCTTGAAGGGGTGTGAAAGAGTGTCTTTTCTAATTGGC	7856
Db	39305	TACGAGGTAGGAGGCAAAATATCTTGAAGGGGTGTGAAAGAGTGTCTTTTCTAATTGGC	39246
Qy	7857	ATGAAGGTGTCAATACAGATTTTGAAGAATTTTAATGGTGCCTTCATTTGGGAATGCTACTGA	7916

[illegible]

Db	38165	AGTGGCTTAGAGGATGCCAGGTCCTTCCATCGAGCCACTGGGTTCCGGGTGCACATTAA	381016
QY	8997	AAAAAAATCTAACCCAGGACATTCAGGAATTCGTAGATTCTGGGAAATCAGTTTCACCATG	9056
Db	38105	AAAAAAATCTAACCCAGGACATTCAGGAATTCGTAGATTCTGGGAAATCAGTTTCACCATG	38046
QY	9057	TTCAAAGAGTCCTTTTTTTTTTTTTTTTTTTTGAGACTCTATTGCCAGGCTGGAGTGCATGGCA	9116
Db	38045	TTCAAAGAGTCCTTTTTTTTTTTTTTTTTTTTGAGACTCTATTGCCAGGCTGGAGTGCATGGCA	37986
QY	9117	TGATCTCGGCTCACTGTAACTCTCGCTCCAGGTTCAAGCGATTCTCCTGTCTCAGCCT	9176
Db	37985	TGATCTCGGCTCACTGTAACTCTCGCTCCAGGTTCAAGCGATTCTCCTGTCTCAGCCT	37926
QY	9177	CCCAAGTACGTGGGATTCACAGGCTGACACCACTGCCCGGCTAAATTTTGTATTTTTAG	9236
Db	37925	CCCAAGTACGTGGGATTCACAGGCTGACACCACTGCCCGGCTAAATTTTGTATTTTTAG	37866
QY	9237	TAGACACAGGTTTCCACCATGTTGGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATC	9296
Db	37865	TAGACACAGGTTTCCACCATGTTGGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATC	37806
QY	9297	CGCTCGCTCGGCCTCCAAAGTCGTGAGATTACAGGTGTAGCCACCTGCCACCGCT	9356
Db	37805	CGCTCGCTCGGCCTCCAAAGTCGTGAGATTACAGGTGTAGCCACCTGCCACCGCT	37746
QY	9357	CAAAAGAGCTTTAAATATATATATCCAGATGGCATGTCTTTACTTTATGTACTACATGCA	9416
Db	37745	CAAAAGAGCTTTAAATATATATATCCAGATGGCATGTCTTTACTTTATGTACTACATGCA	37686
QY	9417	CTTGGCTGCATTAATGTGGTACAGCATCTGTCTTGAAGGCGAGTGCTTCAGGATACC	9476
Db	37685	CTTGGCTGCATTAATGTGGTACAGCATCTGTCTTGAAGGCGAGTGCTTCAGGATACC	37626
QY	9477	ATATACAGCTCAGAAGTTCTCTCTTTAGGCATTAATAATTTAGCAAAAGATATCTCATCTCT	9536
Db	37625	ATATACAGCTCAGAAGTTCTCTCTTTAGGCATTAATAATTTAGCAAAAGATATCTCATCTCT	37566
QY	9537	TCCTTTTAAACCATTCTCTTTTTTGTGGTTAGAAAAGTTATGTAGAAAAAGATTAATGTG	9596
Db	37565	TCCTTTTAAACCATTCTCTTTTTTGTGGTTAGAAAAGTTATGTAGAAAAAGATTAATGTG	37506
QY	9597	ATTAGCTCATTTGTAGAAAAGCTATAAATGAATACAATTTAAAGCTGTTATTAAATTAG	9656
Db	37505	ATTAGCTCATTTGTAGAAAAGCTATAAATGAATACAATTTAAAGCTGTTATTAAATTAG	37446
QY	9657	CCAGTGA AAAAAGCTATTACAACCTTGTCTATTACCTGTTAGTATTATTGTTGCATTA AAAA	9716
Db	37445	CCAGTGA AAAAAGCTATTACAACCTTGTCTATTACCTGTTAGTATTATTGTTGCATTA AAAA	37386
QY	9717	TGCATATACCTTTAATAATGTATTTGTTATGTACTGCATGATTTATTGAAAGTCTTT	9776
Db	37385	TGCATATACCTTTAATAATGTATTTGTTATGTACTGCATGATTTATTGAAAGTCTTT	37326
QY	9777	GTTTCATCTGTGTATATACCTTAATCGCTTTGTGCATTTTGGAGACATTTATTTGCTTCTA	9836
Db	37325	GTTTCATCTGTGTATATACCTTAATCGCTTTGTGCATTTTGGAGACATTTATTTGCTTCTA	37266
QY	9837	ATTTCTCTTACATTTTGTCTTACGGAATATTTTCATTTCAACTGCTGTCGCCGAATTAATCG	9896
Db	37265	ATTTCTCTTACATTTTGTCTTACGGAATATTTTCATTTCAACTGCTGTCGCCGAATTAATCG	37206
QY	9897	TGTTTCTTCACTCTAGGACATTTGCTCTTAAGTTGTAAGACATTTGGTTATTTTACAGC	9956
Db	37205	TGTTTCTTCACTCTAGGACATTTGCTCTTAAGTTGTAAGACATTTGGTTATTTTACAGC	37146
QY	9957	AAACCATCTGAAAGCATATGACAAATATTCTCTCTCTTAATCTTACTATCTGAAAG	10016
Db	37145	AAACCATCTGAAAGCATATGACAAATATTCTCTCTCTTAATCTTACTATCTGAAAG	37086
QY	10017	CAGACTGCTATAAGGCTTCACCTTACTCTCTACCTCATTAAGGAATATGTTACAATTAAT	10076
Db	37085	CAGACTGCTATAAGGCTTCACCTTACTCTCTACCTCATTAAGGAATATGTTACAATTAAT	37026

QY	10077	TATTAGGTAAGCATTTGGTTTTATATTTGGTTTTATTTCACCTGGGCTGAGATTTCAAGAAA	10136
DB	37025	TATTAGGTAAGCATTTGGTTTTATATTTGGTTTTATTTCACCTGGGCTGAGATTTCAAGAAA	36966
QY	10137	CACCCGAGCTCTACAGTAACACATTTTCACTTAACACATTTTACTTAAACATCAGCAACTGTG	10196
DB	36965	CACCCGAGCTCTACAGTAACACATTTTCACTTAACACATTTTACTTAAACATCAGCAACTGTG	36906
QY	10197	GCCTGTTAAATTTTTTAAATAGAAAAATTTAAGTCCTCATTTTCTTTCGGTGTTTTTAAAGC	10256
DB	36905	GCCTGTTAAATTTTTTAAATAGAAAAATTTAAGTCCTCATTTTCTTTCGGTGTTTTTAAAGC	36846
QY	10257	TTAATTTTTCGGCTTTTATTCATAAAATTTCTTAAGGTCAACTACATTTGAAAAATCAAGA	10316
DB	36845	TTAATTTTTCGGCTTTTATTCATAAAATTTCTTAAGGTCAACTACATTTGAAAAATCAAGA	36786
QY	10317	CCTGCATTTTAAATCTTATTACCTCTGGCAAAACCAATTCACAACCATGGTAGTAAAG	10376
DB	36785	CCTGCATTTTAAATCTTATTACCTCTGGCAAAACCAATTCACAACCATGGTAGTAAAG	36726
QY	10377	AGAAGGTCACACCTGGTGGCCATAGGTAAATGTACCACGGTGGTCCGGTCACCAGAGAT	10436
DB	36725	AGAAGGTCACACCTGGTGGCCATAGGTAAATGTACCACGGTGGTCCGGTCACCAGAGAT	36666
QY	10437	GCAGCGCTGAGGGTTTTCTCTGAAGGTAAGGAATAAGAAATGGGTGGAGGGCGTGCAC	10496
DB	36665	GCAGCGCTGAGGGTTTTCTCTGAAGGTAAGGAATAAGAAATGGGTGGAGGGCGTGCAC	36606
QY	10497	GGAATCACTTTAGAGAAAAGCCCTGAAAATTTGAGAAAACAACAAGAACTACTTTA	10556
DB	36605	GGAATCACTTTAGAGAAAAGCCCTGAAAATTTGAGAAAACAACAAGAACTACTTTA	36546
QY	10557	CCAGCTATTTGAAATTCGTGGAATCACAGGCCATTCGTGAGCTGCCTGAACHTGGGAACACA	10616
DB	36545	CCAGCTATTTGAAATTCGTGGAATCACAGGCCATTCGTGAGCTGCCTGAACHTGGGAACACA	36486
QY	10617	ACAGAAGAAAACAACAACCACTCTGATATCATTTAGTGTAAGTACAGCAGGTGATTTAGGA	10676
DB	36485	ACAGAAGAAAACAACAACCACTCTGATATCATTTAGTGTAAGTACAGCAGGTGATTTAGGA	36426
QY	10677	CTGCTGAGAGGTACAGGCCAAAATTCCTATGTTTGTATTTATTAATTAATGTCATCTTATAATA	10736
DB	36425	CTGCTGAGAGGTACAGGCCAAAATTCCTATGTTTGTATTTATTAATTAATGTCATCTTATAATA	36366
QY	10737	CTGTCAGTATTTTATAAAACATTTCTCACAAACTCACACACATTTTAAAAACAACACTG	10796
DB	36365	CTGTCAGTATTTTATAAAACATTTCTCACAAACTCACACACATTTTAAAAACAACACTG	36306
QY	10797	TCTCTAAATCCCAAAATTTTTTTCATAAAC	10825
DB	36305	TCTCTAAATCCCAAAATTTTTTTCATAAAC	36277

RESULT	8	
AAV57926/c		
ID	AAV57926	standard; DNA; 235033 BP.
XX		
AC	AAV57926;	
XX		
DT	23-DEC-1998	(first entry)
XX		
DE		Hereditary haemochromatosis subregion from an unaffected individual.
XX		
KW		Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE;
KW		diagnosis; iron metabolism; NP3; NP4; RoRet; BT1; BT2; BT3;
KW		BT4; BT5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia
KW		type 1 sodium transport gene; ss.

AA	
OS	Homo sapiens.
XX	
PN	WO9814466-A1.
XX	

PD 09-APR-1998.
XX 30-SEP-1997; 97WO-US17658.
XX 07-MAY-1997; 97US-0852495.
PR 01-OCT-1996; 96US-0724394.
XX (PROG-) PROGENITOR INC.
XX Feder JN, Krommal GS, Lauer PM, Ruddy DA, Thomas WJ;
PI Tsuchihashi Z, Wolff RK;
XX WPI; 1998-240014/21.
XX Hereditary haemochromatosis gene products - used to develop products
PT for the diagnosis and treatment of hereditary disorders in iron
PT metabolism
XX Example 2; Fig 8; 209pp; English.
XX The present invention describes hereditary haemochromatosis gene
CC products from the human haemochromatosis gene. The present sequence
CC represents a hereditary haemochromatosis subregion from an individual
CC unaffected by hereditary haemochromatosis (HH). Also described is a
CC method to determine the presence or absence of the common hereditary
CC haemochromatosis (HFE) gene mutation in an individual comprising:
CC (a) providing DNA or RNA from the individual; and (b) assessing the
CC DNA or RNA for the presence or absence of a haplotype or genotype where
CC the presence or absence of the haplotype genotype indicates the likely
CC presence of the HFE gene mutation in the genome of the individual. The
CC HFE gene sequences from the present invention can be used to develop
CC products for use in the diagnosis and treatment of HFE. The present
CC invention also describes BTF genes, which are homologues of the milk
CC protein butyrophilin (BT), and can be used in the production of agonists
CC and antagonists of BT function. Also described are: (1) a RoRet gene
CC which can be used to develop products for the study, diagnosis and
CC treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes
CC which are homologues of a type I sodium transport gene, and can
CC similarly be used for hypophosphatemia.
XX Sequence 235033 BP; 68786 A; 48466 C; 49441 G; 68340 T; 0 other;
SQ

Query Match 28.7%; Score 3109; DB 19; Length 235033;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 10811; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
QY 1 TCTAAGGTTGAGATAAAATTTTAAATGTATGATTGATTTTGAATTCATATAATTTA 60
DB 47148 TCTAAGGTTGAGATAAAATTTTAAATGTATGATTGATTTTGAATTCATATAATTTA 47089
QY 61 AATATCTAAAGTTACAGATCAGAACATTCGGAAGCTACTTTCCCAATCAACACACCCCT 120
DB 47088 AATATCTAAAGTTACAGATCAGAACATTCGGAAGCTACTTTCCCAATCAACACACCCCT 47029
QY 121 TCAGGATTTAAACCAAGGGGACACTGGATCAGCTAGTGTGTTTACAGCAGGTACTCT 180
DB 47028 TCAGGATTTAAACCAAGGGGACACTGGATCAGCTAGTGTGTTTACAGCAGGTACTCT 46969
QY 181 CTGCTGTAGGAGAGAGAGACTAAAGTTCTGAAGACCTGTGTTTCCACAGGAAGTT 240
DB 46968 CTGCTGTAGGAGAGAGAGACTAAAGTTCTGAAGACCTGTGTTTCCACAGGAAGTT 46909
QY 241 TTACTGGGCATCTCTGAGCCTAGCAATAGCTGTAGGGTGACCTTCTGGAGCCATCCCCG 300
DB 46908 TTACTGGGCATCTCTGAGCCTAGCAATAGCTGTAGGGTGACCTTCTGGAGCCATCCCCG 46849
QY 301 TTTCCCGCCCCCAAAAGAGCGAGATTTAAAGGGGACGTGGGCCAGAGCTGGGAA 360
DB 46848 TTTCCCGCCCCCAAAAGAGCGAGATTTAAAGGGGACGTGGGCCAGAGCTGGGAA 46789
QY 361 ATGGGCGCGAGCAGCGCGCT 420

DB 46788 ATGGGCGCGAGCAGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 46729
QY 421 CAGGGCGCTTCTCGCTGAGTCCGAGGGCTCGGGCGCAACTAGGGCGCGCGGGGGTG 480
DB 46728 CAGGGCGCTTCTCGCTGAGTCCGAGGGCTCGGGCGCAACTAGGGCGCGCGGGGGTG 46669
QY 481 GAAAAATCGAAACTAGCTTTTCTTTTGGCTTTGGAGTTTGCTAACTTTGGAGGACCTGC 540
DB 46668 GAAAAATCGAAACTAGCTTTTCTTTTGGCTTTGGAGTTTGCTAACTTTGGAGGACCTGC 46609
QY 541 TCAACCTATCGGAAGCCCTCTCCCTACCTTCTCGCTGAGAGCCCTCGGAGGAGTGC 600
DB 46608 TCAACCTATCGGAAGCCCTCTCCCTACCTTCTCGCTGAGAGCCCTCGGAGGAGTGC 46549
QY 601 CTACCACTCAACTGAGATAGGGTCCCTCGCCAGGAGCTGCCCCCTCCCGGGCTGT 660
DB 46548 CTACCACTCAACTGAGATAGGGTCCCTCGCCAGGAGCTGCCCCCTCCCGGGCTGT 46489
QY 661 CCGGCTCTCGGAGTACTTTTGGAAACCGCCACTCCCTTCCCCCACTAGAATGCTTT 720
DB 46488 CCGGCTCTCGGAGTACTTTTGGAAACCGCCACTCCCTTCCCCCACTAGAATGCTTT 46429
QY 721 TAAATAAATCTCGTAGTCTCTCACTGAGCTGAGCTTAAGCTTGGGGCTCTTGAACCTGG 780
DB 46428 TAAATAAATCTCGTAGTCTCTCACTGAGCTGAGCTTAAAGCTTGGGGCTCTTGAACCTGG 46369
QY 781 AACTCGGGTTTATTTTCCAATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 840
DB 46368 AACTCGGGTTTATTTTCCAATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 46309
QY 841 AGTTTCTTCCCTGAGTGTGTCGCGAGAGGCTGAGCAAAACCCACAGCAGGATCCGACGG 900
DB 46308 AGTTTCTTCCCTGAGTGTGTCGCGAGAGGCTGAGCAAAACCCACAGCAGGATCCGACGG 46249
QY 901 GPTTCCACCTCAGACGAATGTTGGCGGTGGGGCGCGCAAGAGAGTGGGCTTGGGA 960
DB 46248 GPTTCCACCTCAGACGAATGTTGGCGGTGGGGCGCGCAAGAGAGTGGGCTTGGGA 46189
QY 961 TCTGAATTTCTCACCATTCCACCCACTTTTGGTGAGACCTGGGGTGGAGGTCTCTAGGGT 1020
DB 46188 TCTGAATTTCTCACCATTCCACCCACTTTTGGTGAGACCTGGGGTGGAGGTCTCTAGGGT 46129
QY 1021 GAGAGCTCTGAGAGAGGCTTACCTCGGCTTTCCCCACTCTTGGCAATTTCTTTT 1080
DB 46128 GAGAGCTCTGAGAGAGGCTTACCTCGGCTTTCCCCACTCTTGGCAATTTCTTTT 46069
QY 1081 GCCTGGAATAATTAAGTATATGTTAGTTTGAAGTGTGAACTGAACAATTTCTTTTCGG 1140
DB 46068 GCCTGGAATAATTAAGTATATGTTAGTTTGAAGTGTGAACTGAACAATTTCTTTTCGG 46009
QY 1141 CTAGGCTTTATGATTTGCAATGTCTGTGTAATTAAGAGGCTCTCTCAAGTACTGA 1200
DB 46008 CTAGGCTTTATGATTTGCAATGTCTGTGTAATTAAGAGGCTCTCTCAAGTACTGA 45949
QY 1201 TAATGACATGTAAGCAATGCACTCACTTCTAGTTTACATTCATATCTGATCTTATTGA 1260
DB 45948 TAATGACATGTAAGCAATGCACTCACTTCTAGTTTACATTCATATCTGATCTTATTGA 45889
QY 1261 TTTTCACTAGGCATAGGAGGTAGGAGTAAATAATACGTTTATTTTACTAGAAGTTAACT 1320
DB 45888 TTTTCACTAGGCATAGGAGGTAGGAGTAAATAATACGTTTATTTTACTAGAAGTTAACT 45829
QY 1321 GGAATTCAGATTTATTAACCTTTTTCAGTTTCAAAAGACATAAATCTGGTTTCTG 1380
DB 45828 GGAATTCAGATTTATTAACCTTTTTCAGTTTCAAAAGACATAAATCTGGTTTCTG 45769
QY 1381 ATGTATTTCAAGTACTACAGCTGCTTAACTTCTAGTTGACAGTGAATTTGGCCCTGTAG 1440
DB 45768 ATGTATTTCAAGTACTACAGCTGCTTAACTTCTAGTTGACAGTGAATTTGGCCCTGTAG 45709
QY 1441 TGTAGCACAGTGTGTTGGGTACACCGCGGCTCAGCACAGCAGCTTTGAGTTTGGTA 1500
DB 45708 TGTAGCACAGTGTGTTGGGTACACCGCGGCTCAGCACAGCAGCTTTGAGTTTGGTA 45649

QY 1501 CTACGTGTATCCACATTTTACACATGACAGAAATGAGGCATGGCACCGCCTGCTTCCTGG 1560
DB 45648 CTACGTGTATCCACATTTTACACATGACAGAAATGAGGCATGGCACCGCCTGCTTCCTGG 45589
QY 1561 CAAATTTTATCAATGGTACACTGGCTTTGTGTGCAGAGCTCATGTCTCCACTTCATAGC 1620
DB 45588 CAAATTTTATCAATGGTACACTGGCTTTGTGTGCAGAGCTCATGTCTCCACTTCATAGC 45529
QY 1621 TATGATTTCTTAACATCACATGCTCATTTAGAGTTTGAATTAATAAATTTTCAATTTGAGCAG 1680
DB 45528 TATGATTTCTTAACATCACATGCTCATTTAGAGTTTGAATTAATAAATTTTCAATTTGAGCAG 45469
QY 1681 AATATTTCTATTTTACAAAGTGTAAATGAGTCCAGCCATGTTGTCACATGTTCAAGCCC 1740
DB 45468 AATATTTCTATTTTACAAAGTGTAAATGAGTCCAGCCATGTTGTCACATGTTCAAGCCC 45409
QY 1741 CAAGGAGAGCAGGGAACAAGTCTTTACCCCTTTGATATTTTGCATTTCTAGTGGGAGA 1800
DB 45408 CAAGGAGAGCAGGGAACAAGTCTTTACCCCTTTGATATTTTGCATTTCTAGTGGGAGA 45349
QY 1801 GATGACAAATAGCAATGAGCAGAAAGATATACAACTCAGGAATCATGGGTCTGTGA 1860
DB 45348 GATGACAAATAGCAATGAGCAGAAAGATATACAACTCAGGAATCATGGGTCTGTGA 45289
QY 1861 GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGCTGACACTTGAGCAGAGACATGAAGGA 1920
DB 45288 GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGCTGACACTTGAGCAGAGACATGAAGGA 45229
QY 1921 AATAGATGATTTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGCCCTGGCAAG 1980
DB 45228 AATAGATGATTTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGCCCTGGCAAG 45169
QY 1981 TTGGATTTAAAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTGTGGGGGGGGGG 2040
DB 45168 TTGGATTTAAAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTGTGGGGGGGGGG 45109
QY 2041 CGCGTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGCTAGCAGTATTCCTGT 2100
DB 45108 CGCGTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGCTAGCAGTATTCCTGT 45049
QY 2101 CCTCCTACTCACTAGGTGCTAGGAGCACTCCCCAGTCTTGACAACCAAAATGTCTCT 2160
DB 45048 CCTCCTACTCACTAGGTGCTAGGAGCACTCCCCAGTCTTGACAACCAAAATGTCTCT 44989
QY 2161 AAACTTTGGCCATGTCACCTAGTAGACAAACTCCTCGTTAAGAGCTCGGGTTGAAAAA 2220
DB 44988 AAACTTTGGCCATGTCACCTAGTAGACAAACTCCTCGTTAAGAGCTCGGGTTGAAAAA 44929
QY 2221 AATAAACAGTAGTGTGGGAGTAGAGGCCAAGAGTAGTAAATGGCTCAGAGAGGA 2280
DB 44928 AATAAACAGTAGTGTGGGAGTAGAGGCCAAGAGTAGTAAATGGCTCAGAGAGGA 44869
QY 2281 GCCAACAACAGTTGTGCAGCGCCTGTAGGCTGTGGTGTGAATTTAGCCAAAGGAGTA 2340
DB 44868 GCCAACAACAGTTGTGCAGCGCCTGTAGGCTGTGGTGTGAATTTAGCCAAAGGAGTA 44809
QY 2341 ACAGTGATCTGCACAGGCTTTAAAGATTCCTCTGCTGCTATGTGGAAGCAGAAATG 2400
DB 44808 ACAGTGATCTGCACAGGCTTTAAAGATTCCTCTGCTGCTATGTGGAAGCAGAAATG 44749
QY 2401 AAGGGAGCAACAGTAAAGCAGGGAGCCAGCCAGGAAGCTGTTACACAGTCCAGGCAAG 2460
DB 44748 AAGGGAGCAACAGTAAAGCAGGGAGCCAGCCAGGAAGCTGTTACACAGTCCAGGCAAG 44689
QY 2461 AGGTAGTGAGTGGCTGGTGGGACAGAAAGGGAGTGACAAACCATGCTCTCCTGAA 2520
DB 44688 AGGTAGTGAGTGGCTGGTGGGACAGAAAGGGAGTGACAAACCATGCTCTCCTGAA 44629
QY 2521 TATATTTCTGAAGGAAGTCTCTGAAGGATTTCTATGTTGTGAGAGAAAGAGAAATTTGG 2580
DB 44628 TATATTTCTGAAGGAAGTCTCTGAAGGATTTCTATGTTGTGAGAGAAAGAGAAATTTGG 44569

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QY 2641 GTTCAAGACCAAGCTTGGGCAACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA 2700
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Db 36349 TAAATCCCAAAATTTTCATAAAC 36325

RESULT 9
AA96769
ID AAA96769 standard; cDNA; 2506 BP.
XX AC AAA96769;
XX DT 19-FEB-2001 (first entry)
XX DE cDNA sequence encoding a histocompatibility iron loading (HFE) protein.
XX KW Human; histocompatibility iron loading protein; HFE protein;
XX KW major histocompatibility complex; non-classical class I gene;
XX KW chromosome 6p; iron disorder; haemochromatosis; ss.
XX OS Homo sapiens.
XX FH Key
XX CDS 1..1044
FT /tag= a
FT /product= "histocompatibility iron loading (HFE) protein"
FT /tag= b
FT 1..66
FT /tag= 187
FT /tag= C
FT /note= "if this base is mutated to G, then the
FT protein contains the mutation H63D"
FT sig_peptide
FT mutation
FT 193
FT /tag= d
FT /note= "if this base is mutated to T, then the
FT protein contains the mutation S65C"
FT mutation
FT 277
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FT /tag= e
FT /note= "if this base is mutated to C, then the
FT protein contains the mutation G93R"
FT 314
FT /tag= f
FT /note= "if this base is mutated to C, then the
FT protein contains the mutation I105T, which
FT is associated with an iron overload disorder"
XX PN WO200058515-A1.
XX XX
XX PD 05-OCT-2000.
XX XX
XX PF 24-MAR-2000; 2000WO-US07982.
XX XX
XX PR 26-MAR-1999; 99US-0277457.
XX XX
XX PA (BILL-) BILLUPS-ROTHENBERG INC.
XX XX
XX PI Rothenberg BE, Sawada-Hirai R, Barton JC;
XX XX
XX WPI: 2000-647244/62.
XX P-PSDB; AAB19149.
XX XX
XX PT Diagnosing an iron disorder e.g. hemochromatosis or a genetic
XX susceptibility to develop it, by determining the presence of a mutation
XX in exon 2 or an intron of a histocompatibility iron loading nucleic
XX acid.
XX PS Disclosure; Page 2-3; 55pp; English.
XX XX
XX CC The present sequence encodes a human histocompatibility iron loading
XX (HFE) protein. The HFE gene is a major histocompatibility (MHC)
XX non-classical class I gene located on chromosome 6p. Mutations in the
XX gene lead to iron disorders. The specification describes a method for
XX diagnosing an iron disorder or a genetic susceptibility to develop the
XX disorder in a mammal. The method comprises determining the presence of
XX a mutation in exon 2 or an intron of a HFE gene or protein. The mutation
XX is not a C to G missense mutation at nucleotide 187 of the sequence
XX given in A96769 (Genbank Accession number U60319). The presence of the
XX mutation indicates the disorder or the genetic susceptibility to the
XX disorder. The method is used to diagnose an iron disorder
XX e.g. haemochromatosis, or a genetic susceptibility to develop it.
XX SQ Sequence 2506 BP; 648 A; 552 C; 596 G; 710 T; 0 other;

Query Match 9.7%; Score 1051.6; DB 21; Length 2506;
Best Local Similarity 98.7%; Pred. No. 4.4e-176;
Matches 1060; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 7104 CAGGAGGAGCCATGGGCACTAGCTCTTAGCTGAACGTAGTGACACGACGCTCGACAC 7163
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Db 1004 caagagagagccatggggcactagctcttagctgaacgtagtgacacgacgctcgacag 1063

QY 7164 TCACTGTGGGAGAGACAAAACCTAGAGACTCAAGAGGAGGTGCATTTATAGACTCTTC 7223
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Db 1064 tcactgtgggaagagagacaaaactagactcaagagggagtgcttatgatgactcttc 1123

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Db 1124 atgtttcagagagagtggaacccaataacataagaattgcctgacgaactccttgattta 1183

QY 7284 GCCTTCTCTGTTTCATTTCCCTCAAAAAGATTTCCTCCATTTAGGTTTCTGAGTTCCCTCATG 7343
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QY 8064 TACAATAATTTATGATAGATAGGTACTATTATCCCCATTTCTTTTAAATGAGAAGTG 8123
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QY 8124 AAGTAGCCGGGCGGACGGTGGCTACGCTGTAATCCAGCACCTTTGGGAGGCCA 8177
Db 2024 aagtagccgggcaagtggtcgtcgccctgtgtgtcccgagggtgctgagattgca 2077

RESULT 10
AAV23525
ID AAV23525 standard; mRNA; 2727 BP.
XX AC AAV23525;
XX DT 10-JUL-1998 (first entry)
XX DE Haemochromatosis gene.
XX KW Hereditary haemochromatosis; HC gene; HH identification; diagnosis;
XX KW autosomal recessive disorder; SS.
XX OS Homo sapiens.
XX PN WO9807884-A1.
XX PD 26-FEB-1998.
XX PF 22-AUG-1997; 97MO-AU00539.
XX PR 03-SEP-1996; 96AU-0002083.

PR 23-AUG-1996; 96AU-0001849.
XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
XX PI Busfield F, Cullen LM, Jazwinska EC, Powell LW;
XX WPI; 1998-179064/16.
DR Detection of autosomal recessive disorder - particularly hereditary
PT haemochromatosis, by detecting a mutation in the HC gene
XX Disclosure; Page -: 32pp; English.
XX This sequence represents the haemochromatosis (HC) gene. Mutations in
CC this sequence are detected using the method of the invention. The method
CC is for identifying an individual with hereditary haemochromatosis (HH) or
CC a predisposition to develop HH or to genetically pass on HH to an
CC offspring, comprising isolating a biological sample and amplifying a
CC region of genomic DNA in the biological sample encompassing all or part
CC of the DNA between markers D6S265 and D6S276, and detecting at least one
CC homozygous or heterozygous mutation in a nucleotide within the region.
CC The method can also be used for identifying an individual with an
CC autosomal recessive disorder (ARD) or predisposition to develop and/or
CC genetically pass on an ARD to an offspring, comprising isolating a
CC biological sample from the individual and screening genomic DNA in the
CC sample for the presence of a homozygous or heterozygous mutation in a
CC gene, the normal function of which, is required to prevent progression of
CC the disorder. The method(s) can be used to identify individuals that are
CC homozygous or heterozygous (carriers) for the mutation causing the ARD.
CC Especially the method is used to diagnose HH or predisposition to HH by
CC detecting a Cys282Tyr substitution. Individuals homozygous for this
CC mutation have HH and heterozygotes are potential carriers of the
XX disease.
SQ Sequence 2727 BP; 702 A; 606 C; 660 G; 759 T; 0 other;

Query Match 9.7%; Score 1051.6; DB 19; Length 2727;
Best Local Similarity 98.7%; Pred. NO. 4.5e-176;
Matches 1060; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 7104 CAGGAGGAGCCATGGGCACTACGCTCTTAGCTGAACGTGAGTGACACGACGCTGCAGAC 7163
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 AAC68441
 ID AAC68441 standard; DNA; 517 BP.
 XX AC AAC68441;
 XX AC AAC68441;
 DT 21-FEB-2001 (first entry)
 DE Human hereditary hemochromatosis DNA used for mutation detection.
 XX HH; hereditary hemochromatosis; chelation agent;
 KW T-cell differentiation factor; iron overload; ss.
 XX Homo sapiens.
 OS US6140305-A.
 PN 31-OCT-2000.
 PF 04-APR-1997; 97US-0834497.
 PR 04-APR-1996; 96US-0630912.
 PR 16-APR-1996; 96US-0632673.
 PR 23-MAY-1996; 96US-0652265.
 XX (BIRA) BIO-RAD LAB INC.
 PA Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
 PI Feder JN;
 XX WPI; 2001-006341/01.
 DR
 XX

PT New hereditary hemochromatosis gene products or polypeptides, useful
 PT for treating hereditary hemochromatosis in a patient, and as a metal
 PT chelation agent alleviating iron overload -
 XX Disclosure; Fig 6; 108pp; English.
 XX The present invention relates to hereditary hemochromatosis gene
 CC products. These proteins may be used to treat a patient diagnosed as
 CC having human hemochromatosis disease. It is also useful as a metal
 CC chelation agent or as a T-cell differentiation factor, and for
 CC alleviating iron overload. They may also be used in protein replacement
 CC therapy for individuals having a defective human hemochromatosis gene.
 XX Sequence 517 BP; 127 A; 120 C; 146 G; 124 T; 0 other;
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 Query Match 4.8%; Score 517; DB 22; Length 517;
 Best Local Similarity 100.0%; Pred. No. 3.2e-82;
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 AAC68440
 ID AAC68440 standard; DNA; 517 BP.
 XX AC AAC68440;
 XX AC AAC68440;
 DT 21-FEB-2001 (first entry)
 DE Human hereditary hemochromatosis DNA used for mutation detection.
 XX HH; hereditary hemochromatosis; chelation agent;
 KW T-cell differentiation factor; iron overload; ss.
 XX Homo sapiens.
 OS US6140305-A.
 PN

OTHER INFORMATION: mutation"
OTHER INFORMATION: /note= "Hereditary Hemochromatosis (HH)
OTHER INFORMATION: gene 24d1 allele"
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OTHER INFORMATION: for 24d2(C) allele (SEQ ID NO:41)"
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OTHER INFORMATION: for 24d1(A) allele (SEQ ID NO:21)"
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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis"
OTHER INFORMATION:
OTHER INFORMATION: /label= 24d1
US-08-652-265-3

Query Match 100.0%; Score 10825; DB 3; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10825; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 CTGCTGTAGGAGAGAGAACTAAAGTCTGAAGACCTGTTGCTTTTCCACGAGAGTT 240
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QY 1261 TTTTCACTAGGATAGGAGGTAGGAGCTAAATAACTGTTTATTTTACTAGAAGTTAACT 1320
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QY 1381 ATGTTTATTTCAAGTACTACAGCTGCTTCTTAATCTTGTAGTTGACAGTGAATTTGCCCTGTAG 1440
DB 1381 ATGTTTATTTCAAGTACTACAGCTGCTTCTTAATCTTGTAGTTGACAGTGAATTTGCCCTGTAG 1440

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RESULT 2

US-08-834-497A-3
; Sequence 3, Application US/08834497A
; Patent No. 6140305
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,497A
; FILING DATE: 04-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462

REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
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TOPOLOGY: linear
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US-08-834-497A-3

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RESULT 3

US-09-503-444A-3

; Sequence 3, Application US/09503444A

; Patent No. 6228594

; GENERAL INFORMATION:

; APPLICANT: Thomas, Winston J.

; APPLICANT: Drayna, Dennis T.

; APPLICANT: Feder, John N.

; APPLICANT: Gnirke, Andreas

; APPLICANT: Ruddy, David

; APPLICANT: Tsuchihashi, Zenta

; APPLICANT: Wolff, Roger K.

; TITLE OF INVENTION: Hereditary Hemochromatosis Gene

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect Version 8

; CURRENT APPLICATION DATA:

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> APPLICATION NUMBER: US/09/503,444A
> FILING DATE: 14-FEB-2000
> CLASSIFICATION:
> PRIORITY INFORMATION DATA:
> APPLICATION NUMBER: 08/652,265
> FILING DATE: 23-MAY-1996
> PRIORITY INFORMATION DATA:
> APPLICATION NUMBER: 08/632,673
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> PRIORITY INFORMATION DATA:
> APPLICATION NUMBER: 08/630,912
> FILING DATE: 04-APR-1996
> ATTORNEY/AGENT INFORMATION:
> NAME: Poissant, Brian M.
> REGISTRATION NUMBER: 28,462
> REFERENCE/DOCKET NUMBER: 8907-0088-9999
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: 212-790-9090
> TELEFAX: 212-869-9741
> TELEX: 66141
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Db	3601	ACCCAGGACTGTCTATATGGAAGAAGACAGGACTGCAACTCACCTTCCAAAAATGAGGA	3660
Qy	3661	CCAGACACAGCTCATGGTATGAGTTGATGACGGTGTGGAGCCTGGAACCTCAACATCTGTC	3720
Db	3661	CCAGACACAGCTCATGGTATGAGTTGATGACGGTGTGGAGCCTCAACATCTGTC	3720
Qy	3721	CTCCTACTACAAATGTTTAAGCGCTGTGTCTGTCTCCAGGTTTCACACTCTCTGCACTA	3780
Db	3721	CTCCTACTACAAATGTTTAAGCGCTGTGTCTGTCTCCAGGTTTCACACTCTCTGCACTA	3780
Qy	3781	CTCTTTCATGGGTGCCTCAGACAGGACTTGGTCTTTCCCTTGTGTGAAGCTTTGGGCTA	3840
Db	3781	CTCTTTCATGGGTGCCTCAGACAGGACTTGGTCTTTCCCTTGTGTGAAGCTTTGGGCTA	3840
Qy	3841	CGTGGATGACCAAGCTTTCCTGTCTATGATCATGAGAGTGCCTGTGGAGCCCGCAAC	3900
Db	3841	CGTGGATGACCAAGCTTTCCTGTCTATGATCATGAGAGTGCCTGTGGAGCCCGCAAC	3900
Qy	3901	TCCATGGTTTCCAGTAGAAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCTGAGTCTGAA	3960
Db	3901	TCCATGGTTTCCAGTAGAAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCTGAGTCTGAA	3960
Qy	3961	AGGTTGGGATCACATGTTCACTTGTGACTTCTGAGCTATTATGAAAATCACAAACACAG	4020
Db	3961	AGGTTGGGATCACATGTTCACTTGTGACTTCTGAGCTATTATGAAAATCACAAACACAG	4020
Qy	4021	CAAGGTTATGTGGAGAGGGGGCTCACCTCCTGAGTGTGTGAGAGCTTTTCATCTTTTC	4080
Db	4021	CAAGGTTATGTGGAGAGGGGGCTCACCTCCTGAGTGTGTGAGAGCTTTTCATCTTTTC	4080
Qy	4081	ATGCATCTTGAAGAGAAACAGCTGGAAGTCTCAGGTCTTTGTGGAGCAGGAAACAGGAAG	4140
Db	4081	ATGCATCTTGAAGAGAAACAGCTGGAAGTCTCAGGTCTTTGTGGAGCAGGAAACAGGAAG	4140
Qy	4141	GAATTTGCTTCTGAGATCATTTTGTCTCTGGGATGGTGGAAATAGGGACCTTATTCCTT	4200
Db	4141	GAATTTGCTTCTGAGATCATTTTGTCTCTGGGATGGTGGAAATAGGGACCTTATTCCTT	4200
Qy	4201	TGGTTGCAGTTTAAACAGGCTGGGATTTTCCACAGTCCACACCTTGCAGTCTATCTTG	4260
Db	4201	TGGTTGCAGTTTAAACAGGCTGGGATTTTCCAGAGTCCACACCTTGCAGTCTATCTTG	4260
Qy	4261	GGCTGTGAAATGCAAGAGAACACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGG	4320
Db	4261	GGCTGTGAAATGCAAGAGAACACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGG	4320
Qy	4321	CAGGACACCTTTGAATTTCTGCCCTGCACACTGGATTGTGAGACAGCAGAACCCAGGGCC	4380
Db	4321	CAGGACACCTTTGAATTTCTGCCCTGCACACTGGATTGTGAGACAGCAGAACCCAGGGCC	4380
Qy	4381	TGGCCCAACAAGCTGGAGTGGGAAGGCACAAGATTCTGGGCCAGGCAGAAACAGGGCTAC	4440
Db	4381	TGGCCCAACAAGCTGGAGTGGGAAGGCACAAGATTCTGGGCCAGGCAGAAACAGGGCTAC	4440
Qy	4441	CTGGAGAGGGACTGCCCTGCACAGCTGCAGGAGTTGCTGGAGCTGGGGAGAGTGTTTG	4500
Db	4441	CTGGAGAGGGACTGCCCTGCACAGCTGCAGGAGTTGCTGGAGCTGGGGAGAGTGTTTG	4500

QY	4501	GACCAACAAGGTATGGTGGAAACAACACTTCTGCCCCATACTACTAGTGCAGAGTGGAGG	4560
Db	4501	GACCAACAAGGTATGGTGGAAACAACACTTCTGCCCCATACTACTAGTGCAGAGTGGAGG	4560
QY	4561	AGGTTGCAGGCGACGGAAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTC	4620
Db	4561	AGGTTGCAGGCGACGGAAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTC	4620
QY	4621	TCCAAATTCCTGGGAAGGACTTTCTCAATCCCTAGAGTCTCTACCTTATAAATTGAGATGTA	4680
Db	4621	TCCAAATTCCTGGGAAGGACTTTCTCAATCCCTAGAGTCTCTACCTTATAAATTGAGATGTA	4680
QY	4681	TGAGACGCCACAAGTCATGGGTTTAAATTTCTTCTCCATGCATATGGCTCAAGGGAA	4740
Db	4681	TGAGACGCCACAAGTCATGGGTTTAAATTTCTTCTCCATGCATATGGCTCAAGGGAA	4740
QY	4741	GTGTCTATGGCCCCGTGCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTAA	4800
Db	4741	GTGTCTATGGCCCCGTGCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTAA	4800
QY	4801	AAATTCAGAAATGTCAAGCGCGGCGACGGTGGCTCACCCCTCTAATCCAGCACCTTTGGG	4860
Db	4801	AAATTCAGAAATGTCAAGCGCGGCGACGGTGGCTCACCCCTCTAATCCAGCACCTTTGGG	4860
QY	4861	AGGCGGAGCGGGTGGTCAACAAGTCAGAGTTTGAGACGACCGTACCAACATGGTGAA	4920
Db	4861	AGGCGGAGCGGGTGGTCAACAAGTCAGAGTTTGAGACGACCGTACCAACATGGTGAA	4920
QY	4921	ACCGCTCTCTAAAAAATACAAAAATTAGCTGGTCACAGTCATGCGCACCTGTAGTCCCA	4980
Db	4921	ACCGCTCTCTAAAAAATACAAAAATTAGCTGGTCACAGTCATGCGCACCTGTAGTCCCA	4980
QY	4981	GCTAATTTGGAAGGCTGAGGCGAGGAGCATCGCTTGAACCTGGGAAGCGGAAGTTCACATGA	5040
Db	4981	GCTAATTTGGAAGGCTGAGGCGAGGAGCATCGCTTGAACCTGGGAAGCGGAAGTTCACATGA	5040
QY	5041	GCCAAGATCGCGGCACCTGCACCTCCAGCCTAGGCAGCAGAGTGAGACTCCATCTTFAAAAA	5100
Db	5041	GCCAAGATCGCGGCACCTGCACCTCCAGCCTAGGCAGCAGAGTGAGACTCCATCTTFAAAAA	5100
QY	5101	AAAAAANAANAANAAGAGAAATTCAGAGATCTCAGCTATCATATGAATACCGAGACAA	5160
Db	5101	AAAAAANAANAANAAGAGAAATTCAGAGATCTCAGCTATCATATGAATACCGAGACAA	5160
QY	5161	ATATCAAGTGAAGGCACTTATCAGAGTGAAGAAATCTTTTAGGTTTAAAGTTCTTCTCAT	5220
Db	5161	ATATCAAGTGAAGGCACTTATCAGAGTGAAGAAATCTTTTAGGTTTAAAGTTCTTCTCAT	5220
QY	5221	AGACATAGCAATTAATCCTGAAGCTACCTATCTTACAAGTCCGCTCTTTATAACAATGC	5280
Db	5221	AGACATAGCAATTAATCCTGAAGCTACCTATCTTACAAGTCCGCTCTTTATAACAATGC	5280
QY	5281	CTCCTAGGTTGACCCAGGTGAAACTGACCATCTGTATTCAATCATTTTCAATGCACATAA	5340
Db	5281	CTCCTAGGTTGACCCAGGTGAAACTGACCATCTGTATTCAATCATTTTCAATGCACATAA	5340
QY	5341	AGGCAATTTTATCTATCAGAAACAAAGAACATGGGTAAACAGATATGATATTTACATGTG	5400
Db	5341	AGGCAATTTTATCTATCAGAAACAAAGAACATGGGTAAACAGATATGATATTTACATGTG	5400
QY	5401	AGGAGAACAGCTGATCTGACTCTCTCAAGTGACACTGTGTTAGAGTCCAATCTTAGG	5460
Db	5401	AGGAGAACAGCTGATCTGACTCTCTCAAGTGACACTGTGTTAGAGTCCAATCTTAGG	5460
QY	5461	ACAAAAATGGTCTCTCCTCTAGCTGTTTCTTTTCTGAAAAAGGTTATTTCTCTCTCC	5520
Db	5461	ACAAAAATGGTCTCTCCTCTAGCTGTTTCTTTTCTGAAAAAGGTTATTTCTCTCTCC	5520
QY	5521	AACCTATAGAGAGTGAAGTTTCAGTCTTCTCTGGCAAGGGTAAACAGATCCCCTCTC	5580
Db	5521	AACCTATAGAGAGTGAAGTTTCAGTCTTCTCTGGCAAGGGTAAACAGATCCCCTCTC	5580

Qy	5581	CTCATCCTTCTCTTTCTCTGTCAAAGTGCCCTCCTTTGGTGAAGGTGCACATCAATGTGACC	5640
Dd	5581	CTCATCCTTCTCTTTCTCTGTCAAAGTGCCCTCCTTTGGTGAAGGTGCACATCAATGTGACC	5640
Qy	5641	TCTTCAGTGACCACTCTACAGGTGTCGGGCCCTTGAACACTACTACCCCGAACAATCACCAATG	5700
Dd	5641	TCTTCAGTGACCACTCTACAGGTGTCGGGCCCTTGAACACTACTACCCCGAACAATCACCAATG	5700
Qy	5701	AAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTTCSAACCTTAAGAAGCAATATTG	5760
Dd	5701	AAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTTCSAACCTTAAGAAGCAATATTG	5760
Qy	5761	CCCAATGGGGATGGGACCTACCAAGGCTGGATTAACCTTGGCTGTACCCCCCTGGGGAAGAG	5820
Dd	5761	CCCAATGGGGATGGGACCTACCAAGGCTGGATTAACCTTGGCTGTACCCCCCTGGGGAAGAG	5820
Qy	5821	CAGAGATATACGTACACAGGTGAGCAGCCAGCCCTGGATCAGCCCTCATTTGTGATCTGG	5880
Dd	5821	CAGAGATATACGTACACAGGTGAGCAGCCAGCCCTGGATCAGCCCTCATTTGTGATCTGG	5880
Qy	5881	GGTATGTGACTGATGAGACCGAGAGCTGAGAAAATCTATTGGGGGTTTGAGAGGAGTGGC	5940
Dd	5881	GGTATGTGACTGATGAGACCGAGAGCTGAGAAAATCTATTGGGGGTTTGAGAGGAGTGGC	5940
Qy	5941	TGAGGAGGTAAATTATGGCAGTGAGATGAGGATCTCTCTTTTAGGGGTTGGGCTGAGG	6000
Dd	5941	TGAGGAGGTAAATTATGGCAGTGAGATGAGGATCTCTCTTTTAGGGGTTGGGCTGAGG	6000
Qy	6001	GTGGCAATCAAAGGCTTTAACTTGTCTTTTTCHGTTTTAGAGCCCTCACCGTGTGGCACCC	6060
Dd	6001	GTGGCAATCAAAGGCTTTAACTTGTCTTTTTCHGTTTTAGAGCCCTCACCGTGTGGCACCC	6060
Qy	6061	TAGTCATTGGAGTCATCAGTGGAAATGCTTTTGTGCTCATCTTGTTCATTGGAATTT	6120
Dd	6061	TAGTCATTGGAGTCATCAGTGGAAATGCTTTTGTGCTCATCTTGTTCATTGGAATTT	6120
Qy	6121	TGTTTCATTAATTAAGGAAGAGCGAGGTTCAAGTGAGTGAGGAACAAGGGGGAAGTCTCT	6180
Dd	6121	TGTTTCATTAATTAAGGAAGAGCGAGGTTCAAGTGAGTGAGGAACAAGGGGGAAGTCTCT	6180
Qy	6181	PAGTACCTTCGCCAGGCGACAGTGGGAAGAGGCGAGAGGGGATCTGGCATCCATGGG	6240
Dd	6181	PAGTACCTTCGCCAGGCGACAGTGGGAAGAGGCGAGAGGGGATCTGGCATCCATGGG	6240
Qy	6241	AAGCATTTTTCTCATTTATATCTTTGGGACACCAAGCTCCCTGGGAGACAGAAAAAT	6300
Dd	6241	AAGCATTTTTCTCATTTATATCTTTGGGACACCAAGCTCCCTGGGAGACAGAAAAAT	6300
Qy	6301	AATGGTTCTCCCGCAAGTCTCTAATTCACAACAACATCTTCAGAGCACCTACTAT	6360
Dd	6301	AATGGTTCTCCCGCAAGTCTCTAATTCACAACAACATCTTCAGAGCACCTACTAT	6360
Qy	6361	TTTGAAGAGCTGTTTAAGGTAGTACAGGGGCTTTGAGGTTGAGAACTCAGTGTGGCTAT	6420
Dd	6361	TTTGAAGAGCTGTTTAAGGTAGTACAGGGGCTTTGAGGTTGAGAACTCAGTGTGGCTAT	6420
Qy	6421	TCTCAGAACCCAAATCTGTTAGGAAATGAATGTATAGCAAGTAATGTAGTTAAAGAAG	6480
Dd	6421	TCTCAGAACCCAAATCTGTTAGGAAATGAATGTATAGCAAGTAATGTAGTTAAAGAAG	6480
Qy	6481	ACCCCATGAGTCTTAAAGCAGCAGGAAGCAAAATCTTTAGGGTGTCAAGGAAGAAATG	6540
Dd	6481	ACCCCATGAGTCTTAAAGCAGCAGGAAGCAAAATGCTTTAGGGTGTCAAGGAAGAAATG	6540
Qy	6541	ATCACATTCAGCTGGGGATCAAGATAGCCCTCTGGATCTTGAAGGAGAAAGCTGGATTCCA	6600
Dd	6541	ATCACATTCAGCTGGGGATCAAGATAGCCCTCTGGATCTTGAAGGAGAAAGCTGGATTCCA	6600
Qy	6601	TTAGTGTAGTTGAAGATGATGGGAGGTCTACACACAGCGGCAACCATGCCAAGTAGGA	6660
Dd	6601	TTAGTGTAGTTGAAGATGATGGGAGGTCTACACACAGCGGCAACCATGCCAAGTAGGA	6660
Qy	6661	GAGTATAAGGCACTAGGAGATTTAGAAAATAATTACTGTACCTTTAAACCCCTGAGTTTGGCT	6720
Dd	6661	GAGTATAAGGCACTAGGAGATTTAGAAAATAATTACTGTACCTTTAAACCCCTGAGTTTGGCT	6720
Qy	6721	AGCTATCACTCACCATAATTTATGCAATTTCTACCCCTGAACATCTGTGTGGTGTAGGGAAGA	6780
Dd	6721	AGCTATCACTCACCATAATTTATGCAATTTCTACCCCTGAACATCTGTGTGGTGTAGGGAAGA	6780
Qy	6781	GAATCAGAAAAGAACCCAGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTGGGTATTGA	6840
Dd	6781	GAATCAGAAAAGAACCCAGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTGGGTATTGA	6840
Qy	6841	TCACITGGGGTGTCAATTGAAGGATCCTAAGAAAGAGGAGCAGACTCTCCCTTATATGGTG	6900
Dd	6841	TCACITGGGGTGTCAATTGAAGGATCCTAAGAAAGAGGAGCAGACTCTCCCTTATATGGTG	6900
Qy	6901	AATGTGTTTAAAGAAAGTTAGATGAGAGGTGAGGAGACAGTTTGAAGGCCAATTAGCAT	6960
Dd	6901	AATGTGTTTAAAGAAAGTTAGATGAGAGGTGAGGAGACAGTTTGAAGGCCAATTAGCAT	6960
Qy	6961	TTCCAGATGAGAGATAAATGGTTCTTGAATCCAATAGTSCCCAGGTCTAAATTTGAGATGG	7020
Dd	6961	TTCCAGATGAGAGATAAATGGTTCTTGAATCCAATAGTSCCCAGGTCTAAATTTGAGATGG	7020
Qy	7021	GTGAATGAGGAAAATAAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	7080
Dd	7021	GTGAATGAGGAAAATAAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	7080
Qy	7081	CTTTCTCTGGGTCTTTGCTCCACAGGAGGAGCCATAGTCTCTTACGTGAGTGAACG	7140
Dd	7081	CTTTCTCTGGGTCTTTGCTCCACAGGAGGAGCCATAGTCTCTTACGTGAGTGAACG	7140
Qy	7141	TGAGTGACACGCGAGCTCGAGACTCACTGTGGGAAGGAGACAAAACTTAGAGACTCAAGA	7200
Dd	7141	TGAGTGACACGCGAGCTCGAGACTCACTGTGGGAAGGAGACAAAACTTAGAGACTCAAGA	7200
Qy	7201	GGAGTGCACTTTATGAGCTCTTCATGTTTTCAGGAGAGAGTTGAACCTTAACATAGAAAT	7260
Dd	7201	GGAGTGCACTTTATGAGCTCTTCATGTTTTCAGGAGAGAGTTGAACCTTAACATAGAAAT	7260
Qy	7261	GGCTGACGAACTCCTTGATTGATTCCTCTGTTTCATTTCTCTCAAAAAAGATTTCCCAT	7320
Dd	7261	GGCTGACGAACTCCTTGATTGATTCCTCTGTTTCATTTCTCTCAAAAAAGATTTCCCAT	7320
Qy	7321	TTAGGTTTCTGAGTTCTCTGCATGCCGGTGATCCCTGAGCTGTGACCTCTCCCTGGAACTG	7380
Dd	7321	TTAGGTTTCTGAGTTCTCTGCATGCCGGTGATCCCTGAGCTGTGACCTCTCCCTGGAACTG	7380
Qy	7381	TCTCTCATCAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCCTCGCTCACTCAGAG	7440
Dd	7381	TCTCTCATCAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCCTCGCTCACTCAGAG	7440
Qy	7441	ACATACACCTATGTCATTTCAITTTTCTATTTTGGAGAGGAGTCCCTTAAATTTGGGGGA	7500
Dd	7441	ACATACACCTATGTCATTTCAITTTTCTATTTTGGAGAGGAGTCCCTTAAATTTGGGGGA	7500
Qy	7501	CTTACATGATTCATTTTAAACATCTGAGAAAAGCTTTGAACCCCTGGGACGTGGCTAGTFCAT	7560
Dd	7501	CTTACATGATTCATTTTAAACATCTGAGAAAAGCTTTGAACCCCTGGGACGTGGCTAGTFCAT	7560
Qy	7561	AACCTTTACCAGATTTTTTACACATGTATCTATGCAATTTTCTGGACCCGTTCAACTTTTCCT	7620
Dd	7561	AACCTTTACCAGATTTTTTACACATGTATCTATGCAATTTTCTGGACCCGTTCAACTTTTCCT	7620
Qy	7621	TTGAATTCCTCTCTCTGTGTGTACCAGTAACTCATCTGTCTACCAAGCCTTTGGGATTTCTTC	7680
Dd	7621	TTGAATTCCTCTCTCTGTGTGTACCAGTAACTCATCTGTCTACCAAGCCTTTGGGATTTCTTC	7680
Qy	7681	CATCTCATTTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACCAATGGAAGAG	7740
Dd	7681	CATCTCATTTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACCAATGGAAGAG	7740
Qy	7741	GCACCTGTCCCAAGAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGGTGTTTTTAGC	7800
Dd	7741	GCACCTGTCCCAAGAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGGTGTTTTTAGC	7800

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Db 9961 CATTCTGAAGCATATGACAAATATTCTCTCTTAATATCTTACTATACTGAAAGCAGA 10020
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RESULT 4
US-08-652-265-1
; Sequence 1, Application US/08652265
; Patent No. 6025130
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchinashi, Zenta
; APPLICANT: Wolff, Roger K.
```

```
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 17957-000500
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
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; LENGTH: 10825 base pairs
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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; LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
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; OTHER INFORMATION: /label= 24dl
US-08-652-265-1

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Matches 10824; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 5

US-08-652-265-7
Sequence 7, Application US/08652265
Patent No. 6025130
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchinashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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US-08-652-265-7

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 10824; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 10141 CCAGTCTTCAAGTAACACATTTTCACTAACACATTTTACTAAACATCAGCACTGTGSCCT 10200
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RESULT 6

US-08-834-497A-1
; Sequence 1, Application US/08834497A
; Patent No. 6140305
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gairke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,497A
; FILING DATE: 04-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0056-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:

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RESULT 7

; Sequence 7, Application US/08834497A
; Patent No. 6140305
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: PastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNTE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: 6040..6153, 7107..7147)
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NAME/KEY: allele
LOCATION: replace(3872, "g")
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US-08-834-497A-7

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Query Match 100.0%; Score 10823.4; DB 4; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10824: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; Patent No. 6228594
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect Version 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,444A
; FILING DATE: 14-Feb-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/652,265
; FILING DATE: 23-May-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,673
; FILING DATE: 16-Apr-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,912
; FILING DATE: 04-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0088-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
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; US-09-503-444A-1

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RESULT 9
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; Sequence 7, Application US/09503444A
; Patent No. 6228594
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect Version 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,444A
; FILING DATE: 14-Feb-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/652,265
; FILING DATE: 23-May-1996
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0088-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741

INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10825 base pairs
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0-503-444A-7

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 10824; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 10
US-08-724-394A-20
; Sequence 20, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston

; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
; US-08-724-394A-20

Query Match 100.0%; Score 10823.4; DB 2; Length 246240;
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Matches 10824; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21

Query Match 100.0%; Score 10823.4; DB 2; Length 246240;
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Matches 10824; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 12
US-08-724-394A-22
; Sequence 22, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereof
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"

US-08-724-394A-22

Query Match 100.0%; Score 10823.4; DB 2; Length 246240;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 10824; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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; GENERAL INFORMATION:
; Patent No. 6025130
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gniirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 17957-000500
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10825 base pairs
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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US-08-652-265-5

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Q	y	10081	AGGTAAAGCATTTGTTTATATATGTTTATTTTACCTTGGGCTGAGATTTCAAGAAAAACCC	10140
D	b	10081	AGGTAAAGCATTTGTTTATATATGTTTATTTTACCTTGGGCTGAGATTTCAAGAAAAACCC	10140
Q	y	10141	CSAGTCTTTCACAGTAACACATTTCACTAACACATTTACTAAACATCATGACACTGTGGCCT	10200
D	b	10141	CSAGTCTTTCACAGTAACACATTTCACTAACACATTTACTAAACATCATGACACTGTGGCCT	10200
Q	y	10201	GTTAATTTTTTAAATAGAAAATTTTAAGTCCCTCATTTCTTTCGGTGGTTTTTAAAGCTTAA	10260
D	b	10201	GTTAATTTTTTAAATAGAAAATTTTAAGTCCCTCATTTCTTTCGGTGGTTTTTAAAGCTTAA	10260
Q	y	10261	TTTTTCTCGCTTTATTCATAAATCTTAAAGTCAACTACATTTGAAAAATCAAAAGACCTG	10320
D	b	10261	TTTTTCTCGCTTTATTCATAAATCTTAAAGTCAACTACATTTGAAAAATCAAAAGACCTG	10320
Q	y	10321	CATTTTAAATTTCTTATTACCTCTGGCAAAACCAFTCAACAACCATGCTAGTAAAGAGAA	10380
D	b	10321	CATTTTAAATTTCTTATTACCTCTGGCAAAACCAFTCAACAACCATGCTAGTAAAGAGAA	10380
Q	y	10381	GGGTGACACCTGGTGGCCATAGGTAAATGTACCAGGTTGGTCCGGTGACCAAGATGCAG	10440
D	b	10381	GGGTGACACCTGGTGGCCATAGGTAAATGTACCAGGTTGGTCCGGTGACCAAGATGCAG	10440
Q	y	10441	CGCTGAGGGTTTTCTGTAAGGTAAAAGGAATAAGAAATGGGTGGAGGGCGCTGCACCTGGAA	10500
D	b	10441	CGCTGAGGGTTTTCTGTAAGGTAAAAGGAATAAGAAATGGGTGGAGGGCGCTGCACCTGGAA	10500
Q	y	10501	ATCACCTGTGAGAAAAGCCCCGTGAAAATTTGAGAAAAACAAAGAACTACTTTACCAG	10560
D	b	10501	ATCACCTGTGAGAAAAGCCCCGTGAAAATTTGAGAAAAACAAAGAACTACTTTACCAG	10560
Q	y	10561	CTATTTGAATTCGCTGGAATCAAGGCCATTTGCTGAGCTGCCTGAACCTGGGAACACAAACAG	10620
D	b	10561	CTATTTGAATTCGCTGGAATCAAGGCCATTTGCTGAGCTGCCTGAACCTGGGAACACAAACAG	10620
Q	y	10621	AAGGAAAAACAACCACTCTGTAATCATTTAGTCAAGTACAGCAAGTGAATTCAGGACTGC	10680
D	b	10621	AAGGAAAAACAACCACTCTGTAATCATTTAGTCAAGTACAGCAAGTGAATTCAGGACTGC	10680
Q	y	10681	TGAGAGGTACAGGCCAAAATTTCTTATGTTGTTATTAATAATGTCATCTTATAAATCTGT	10740
D	b	10681	TGAGAGGTACAGGCCAAAATTTCTTATGTTGTTATTAATAATGTCATCTTATAAATCTGT	10740
Q	y	10741	CAGTATTTTTATAAACATTTCTTCACAACTCACACATTTTAAAAACAACAACTGCTCTC	10800
D	b	10741	CAGTATTTTTATAAACATTTCTTCACAACTCACACATTTTAAAAACAACAACTGCTCTC	10800
Q	y	10801	TAAAAATCCCCAAATTTTTTCATTAAC	10825
D	b	10801	TAAAAATCCCCAAATTTTTTCATTAAC	10825

QY 721 TAAATAAATCTCGTAGTTCCTCACCTGAGCTGAGCTAAGCCTGGGGCTCCTTGAACCTGG 780
DB 721 TAAATAAATCTCGTAGTTCCTCACCTGAGCTGAGCTAAGCCTGGGGCTCCTTGAACCTGG 780
QY 781 AACTCGGGTTTATTTCCCAATGTCAGCTGTCAGATTTTCCCAAGTCACTCCCAACAGG 840
DB 781 AACTCGGGTTTATTTCCCAATGTCAGCTGTCAGATTTTCCCAAGTCACTCCCAACAGG 840
QY 841 AAGTCTTCCCTGAGTGTGTCGCGAGAAGGCTGAGCAAAACCCACAGCAGGATCCGCACGG 900
DB 841 AAGTCTTCCCTGAGTGTGTCGCGAGAAGGCTGAGCAAAACCCACAGCAGGATCCGCACGG 900
QY 901 GGTTCACCACTCAGAACCAATGCGTTGGCGGTGGGGCGCGAAGAGTGCGGTGGGGA 960
DB 901 GGTTCACCACTCAGAACCAATGCGTTGGCGGTGGGGCGCGAAGAGTGCGGTGGGGA 960
QY 961 TCTGAATCTTCCACCACTTCCACCACTTTTGGTGAGACCTGGGTGGAGGCTCTAGGCT 1020
DB 961 TCTGAATCTTCCACCACTTCCACCACTTTTGGTGAGACCTGGGTGGAGGCTCTAGGCT 1020
QY 1021 GGGAGGCTCCTGAGAGGCGCTACCTCGGGCTTTTCCCACTCTTGGCAATGTTCTTTT 1080
DB 1021 GGGAGGCTCCTGAGAGGCGCTACCTCGGGCTTTTCCCACTCTTGGCAATGTTCTTTT 1080
QY 1081 GCTCGGAAATTAAGTATATGTTAGTTTGAACGTTTGAACCTGAACATTTCTTTTCGG 1140
DB 1081 GCTCGGAAATTAAGTATATGTTAGTTTGAACGTTTGAACCTGAACATTTCTTTTCGG 1140
QY 1141 CTAGGCTTTATTTGATTTGCAATGTCTGTGTAATTAAGAGGCCCTCTACAAACTCTGA 1200
DB 1141 CTAGGCTTTATTTGATTTGCAATGTCTGTGTAATTAAGAGGCCCTCTACAAACTCTGA 1200
QY 1201 TAATGAACATGTAAGCAATGACACCTCTCAAGTTTCAATTCATATCTGATCTTATTTGA 1260
DB 1201 TAATGAACATGTAAGCAATGACACCTCTCAAGTTTCAATTCATATCTGATCTTATTTGA 1260
QY 1261 TTTTCACCTAGCATTAGGAGCTAGGAGCTAATATAGCTTTTATTTACTAGAAGTTAACT 1320
DB 1261 TTTTCACCTAGGAGCTAGGAGCTAATATAGCTTTTATTTACTAGAAGTTAACT 1320
QY 1321 GGAATTCAGATTATATACTCTTTTCAGTTTACAAAGAACATAAATATCTGTTTCTG 1380
DB 1321 GGAATTCAGATTATATACTCTTTTCAGTTTACAAAGAACATAAATATCTGTTTCTG 1380
QY 1381 ATGTTATTTCAAGTACTACACCTGCTTCAATCTTGTAGTGTGACGTGATTTTGCCTGTAG 1440
DB 1381 ATGTTATTTCAAGTACTACACCTGCTTCAATCTTGTAGTGTGACGTGATTTTGCCTGTAG 1440
QY 1441 TGTAGCAGATGTTCTGTGGGTACACCGCGCTCAGCAGCAGCATTGAGTTTTCGTA 1500
DB 1441 TGTAGCAGATGTTCTGTGGGTACACCGCGCTCAGCAGCAGCATTGAGTTTTCGTA 1500
QY 1501 CTACGTGTATCCACATTTTACACATGACAAGATGAGGATGGCAGCGCTGCTTCCTGG 1560
DB 1501 CTACGTGTATCCACATTTTACACATGACAAGATGAGGATGGCAGCGCTGCTTCCTGG 1560
QY 1561 CAAATTTTATTTCAATGTTACATGCGCTTTGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620
DB 1561 CAAATTTTATTTCAATGTTACATGCGCTTTGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620
QY 1621 TATGATTTTAAACATCAGCTGATTTAGAGTTTGAATAATAAATTTCAATTTGAGCAG 1680
DB 1621 TATGATTTTAAACATCAGCTGATTTAGAGTTTGAATAATAAATTTCAATTTGAGCAG 1680
QY 1681 AAATATTCATTTTACAAAGTAAATGAGTCCAGCCATGTGTGACACGTTTCAAGCC 1740
DB 1681 AAATATTCATTTTACAAAGTAAATGAGTCCAGCCATGTGTGACACGTTTCAAGCC 1740
QY 1741 CAAGGGAGAGCAGGGAACAGCTTTTACCTTTGATATTTTGGATTTTCTAGTGGGAGA 1800
DB 1741 CAAGGGAGAGCAGGGAACAGCTTTTACCTTTGATATTTTGGATTTTCTAGTGGGAGA 1800
QY 1801 GATGACAATAAGCAATGAGCAGAGAAGATATACAACATCAGGAATCATGGGTGTTGTGA 1860

DB 1801 GATGACAATAAGCAATGAGCAGAGAAGATATACAACATCAGGAATCATGGGTGTTGTGA 1860
QY 1861 GAAGCAGAGAAGTCAGGGCAAGTCACCTCTGGGCTGACACTTGGAGAGACATGAAGGA 1920
DB 1861 GAAGCAGAGAAGTCAGGGCAAGTCACCTCTGGGCTGACACTTGGAGAGACATGAAGGA 1920
QY 1921 AATAAGAAATCATATTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGCCTGCAAG 1980
DB 1921 AATAAGAAATCATATTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGCCTGCAAG 1980
QY 1981 TTGGATTTAAAGCGGTTTCTCAGCAGTACTCATGTGTGTGTGTGTGGGGGGGGGG 2040
DB 1981 TTGGATTTAAAGCGGTTTCTCAGCAGTACTCATGTGTGTGTGTGTGGGGGGGGGG 2040
QY 2041 CGGCGTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCCTGT 2100
DB 2041 CGGCGTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCCTGT 2100
QY 2101 CCTCCCTACTCAGTGTAGGAGCAGTCCGCCAGTCTTGACAAACCAAAATGTCTCT 2160
DB 2101 CCTCCCTACTCAGTGTAGGAGCAGTCCGCCAGTCTTGACAAACCAAAATGTCTCT 2160
QY 2161 AAATTTTCCACATGTACCTAGTAGCAAACTCCTGGTTAAGAAGCTCGGGTTGAAAA 2220
DB 2161 AAATTTTCCACATGTACCTAGTAGCAAACTCCTGGTTAAGAAGCTCGGGTTGAAAA 2220
QY 2221 AATAAACAAGTACTGTGGGAGTAGAGCCCAAGAGTAGTAAATGGGCTCAGAGAGGA 2280
DB 2221 AATAAACAAGTACTGTGGGAGTAGAGCCCAAGAGTAGTAAATGGGCTCAGAGAGGA 2280
QY 2281 GCCACAAACAAGTTGTGAGGCGCTGTAGGCTGTGGTGTGAATTTCTAGCCAAAGGATG 2340
DB 2281 GCCACAAACAAGTTGTGAGGCGCTGTAGGCTGTGGTGTGAATTTCTAGCCAAAGGATG 2340
QY 2341 ACAGTGTATCTGTACAGGCTTTTAAAGATGTCTCTGGTGTCTATGTGGAAGCAGAAATG 2400
DB 2341 ACAGTGTATCTGTACAGGCTTTTAAAGATGTCTCTGGTGTCTATGTGGAAGCAGAAATG 2400
QY 2401 AAGGGAGCAACAGTAAAGCAGGAGCCAGCCAGCAAGAGCTGTACACAGTCCAGGCAAG 2460
DB 2401 AAGGGAGCAACAGTAAAGCAGGAGCCAGCCAGCAAGAGCTGTACACAGTCCAGGCAAG 2460
QY 2461 AGTGTAGTGGTGGGTGGGACAGAAAAGGAGTGACAAACCATTTGTCTCTCTGAA 2520
DB 2461 AGTGTAGTGGTGGGTGGGACAGAAAAGGAGTGACAAACCATTTGTCTCTCTGAA 2520
QY 2521 TATATTCTGAAGGAAGTTGCTGAGGATTTCTATGTTGTGTGAGAGAAAGAGAAATGG 2580
DB 2521 TATATTCTGAAGGAAGTTGCTGAGGATTTCTATGTTGTGTGAGAGAAAGAGAAATGG 2580
QY 2581 CTGGGTGTAGTGTATGCTCAAGGAGGAGCCCAAGGAGAGATTCCTGAGCTCAGGA 2640
DB 2581 CTGGGTGTAGTGTATGCTCAAGGAGGAGCCCAAGGAGAGATTCCTGAGCTCAGGA 2640
QY 2641 GTTCAAGACAGCCTGGGCAACACAGAAAACCCCTTCTTACAAAAATACAAAAATTA 2700
DB 2641 GTTCAAGACAGCCTGGGCAACACAGAAAACCCCTTCTTACAAAAATACAAAAATTA 2700
QY 2701 GCTGGGTGTGGTGGCATGCACCTGTGATCCTAGTACTCGGGAGGCTGAGGTGGAGGTA 2760
DB 2701 GCTGGGTGTGGTGGCATGCACCTGTGATCCTAGTACTCGGGAGGCTGAGGTGGAGGTA 2760
QY 2761 TTGCTTTGAGCCAGGAAGTTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 2820
DB 2761 TTGCTTTGAGCCAGGAAGTTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 2820
QY 2821 CTAGGTGACAGAGCAAGCCCTGTCTCCCTGACCCCTGAAAAAGAGAGAGTAAAGT 2880
DB 2821 CTAGGTGACAGAGCAAGCCCTGTCTCCCTGACCCCTGAAAAAGAGAGAGTAAAGT 2880
QY 2881 TGACTTTGTCTTTTATTTTAAATTTTATTTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 2940

QY 5101 AAAAAAAAAAAAAAGAGAAATTCAGAGATCTCAGCATATCATATGAATACACGACAAA 5160
Db 5101 AAAAAAAAAAAAAAGAGAAATTCAGAGATCTCAGCATATCATATGAATACACGACAAA 5160
QY 5161 ATATCAAGTGAGCCACTTATCAGACTAGAGAAATCCTTTAGGTTAAAGATTCTTTTCAT 5220
Db 5161 ATATCAAGTGAGCCACTTATCAGAGTAGAGAAATCCTTTAGGTTAAAGATTCTTTTCAT 5220
QY 5221 AGAACAATAGCAATATATCACTGAAGCTTACCTATCTTACAAGTCCGCTCTTATAACAATGC 5280
Db 5221 AGAACAATAGCAATATATCACTGAAGCTTACCTATCTTACAAGTCCGCTCTTATAACAATGC 5280
QY 5281 CTCCTAGTTGACCCAGGTGAACATGACCATCTGTATTCATATTCATATTCATAGCATATA 5340
Db 5281 CTCCTAGTTGACCCAGGTGAACATGACCATCTGTATTCATATTCATATTCATAGCATATA 5340
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Db 5341 AGGGCAATTTATCTATCATCAGAACAAAGACATGGGTACAGATATCTATTTACATGTG 5400
QY 5401 AGGAGAACAAAGCTGATCTGACTGCTCTCAAGTGACACTGTGTAGAGTCCAAATCTTAGG 5460
Db 5401 AGGAGAACAAAGCTGATCTGACTGCTCTCAAGTGACACTGTGTAGAGTCCAAATCTTAGG 5460
QY 5461 ACACAAAATGGTGTCTCTCCTGTAGCTGTGTTTTTTCTGAAAAGGGTATTTCCCTTCCTCC 5520
Db 5461 ACACAAAATGGTGTCTCTCCTGTAGCTGTGTTTTTTCTGAAAAGGGTATTTCCCTTCCTCC 5520
QY 5521 AACCTATAGAAGGAAGTGAAGCTCCAGTCTCCAGTGCCTTTGGTGAAGGTGACACATCATGTGACC 5580
Db 5521 AACCTATAGAAGGAAGTGAAGCTCCAGTCTCCAGTGCCTTTGGTGAAGGTGACACATCATGTGACC 5580
QY 5581 CTCATCCTTCCCTTTCCCTGTCCTCAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACC 5640
Db 5581 CTCATCCTTCCCTTTCCCTGTCCTCAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACC 5640
QY 5641 TCTTCAGTGACCACTCTACGGTGTGGGCTTGAACACTACCCCCAGAACATACACCATG 5700
Db 5641 TCTTCAGTGACCACTCTACGGTGTGGGCTTGAACACTACCCCCAGAACATACACCATG 5700
QY 5701 AAGTGTGCTGAAGGATAAGCAGCAATGGATGCCAAGGAGTTCGAACCTTAAAGACGTATTG 5760
Db 5701 AAGTGTGCTGAAGGATAAGCAGCAATGGATGCCAAGGAGTTCGAACCTTAAAGACGTATTG 5760
QY 5761 CCCAATGGGGATGGGACCTTACCAGGCTGGATAAOCCTTGGCTGTACCCCTGGGGAAGAG 5820
Db 5761 CCCAATGGGGATGGGACCTTACCAGGCTGGATAAOCCTTGGCTGTACCCCTGGGGAAGAG 5820
QY 5821 CAGAGATATACGTACAGGTGGAGCACCCAGGCTGGATFCAGCCCTCATTTGTATCTGG 5880
Db 5821 CAGAGATATACGTACAGGTGGAGCACCCAGGCTGGATFCAGCCCTCATTTGTATCTGG 5880
QY 5881 GGTATGTGACTGATGAGCCAGGAGCTGAGAAAATCTATTTGGGGGTTGAGAGGAGTGCC 5940
Db 5881 GGTATGTGACTGATGAGCCAGGAGCTGAGAAAATCTATTTGGGGGTTGAGAGGAGTGCC 5940
QY 5941 TGAGGAGGTAATATATGGCAGTGAGATGAGCATCTGCTCTTTGTTAGGGGTTGGGCTGAGG 6000
Db 5941 TGAGGAGGTAATATATGGCAGTGAGATGAGCATCTGCTCTTTGTTAGGGGTTGGGCTGAGG 6000
QY 6001 GTGGCAATCAAAAGGCTTTAACTTGTCTTTCTGTTTTAGAGCCCTCACCGTCTGGCACCC 6060
Db 6001 GTGGCAATCAAAAGGCTTTAACTTGTCTTTCTGTTTTAGAGCCCTCACCGTCTGGCACCC 6060
QY 6061 TAGTCATTTGAGTCAATCAGTGAATTTGCTGTTTTTGTGCTCATCTTGTTCATTTGAATTT 6120
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QY 6121 TGTTCATATATTAAGGAAGAGCAGGGTTCAAGTGAGTAGGAACAAGGGGGAAGTCTCT 6180
Db 6121 TGTTCATATATTAAGGAAGAGCAGGGTTCAAGTGAGTAGGAACAAGGGGGAAGTCTCT 6180
QY 6181 TAGTACCTCTGCCCCAGGCACAGTGGGAAGAGGGGACAGAGGGGATCTGGCATCCATGGG 6240

Db 6181 TAGTACCTCTGCCCCAGGCACAGTGGGAAGAGGGGACAGAGGGGATCTGGCATCCATGGG 6240
QY 6241 AAGCATTTTCTCATTTATATCTTTGGGACACACAGCTCCCTGGGAGACAGAAAAT 6300
Db 6241 AAGCATTTTCTCATTTATATCTTTGGGACACACAGCTCCCTGGGAGACAGAAAAT 6300
QY 6301 AATGGTCTCTCCCAAGATGAAAGTCTCTAATTCACAAAACATCTTCAGACACCTACTAT 6360
Db 6301 AATGGTCTCTCCCAAGATGAAAGTCTCTAATTCACAAAACATCTTCAGACACCTACTAT 6360
QY 6361 TTTGCAAGAGCTGTTTAAAGTAGTAGAGGGCTTTAGGTTGAGAAGTCACTGTGGCTAT 6420
Db 6361 TTTGCAAGAGCTGTTTAAAGTAGTAGAGGGCTTTAGGTTGAGAAGTCACTGTGGCTAT 6420
QY 6421 TCTCAGAACCCAAATCTGGTAGGGAATCAATTCATAGCAAGTAAATGTAGTTAAAGAAG 6480
Db 6421 TCTCAGAACCCAAATCTGGTAGGGAATGAAATGTAGCAAGTAAATGTAGTTAAAGAAG 6480
QY 6481 ACCCATGAGGTCTTAAGCAGGAGGAGCAATGCTTAGGGTGTCAAAAGGAAAGATG 6540
Db 6481 ACCCATGAGGTCTTAAGCAGGAGGAGCAATGCTTAGGGTGTCAAAAGGAAAGATG 6540
QY 6541 ATCACATTCAGCTGGGATCAAGATAGCCTTCTGGATCTTTGAAGGAGAAAGCTGGATTCCA 6600
Db 6541 ATCACATTCAGCTGGGATCAAGATAGCCTTCTGGATCTTTGAAGGAGAAAGCTGGATTCCA 6600
QY 6601 TTAGGTGAGGTTGAAGATGATGGGAGGTCTACACAGACGGAGCAACCATGCCAAGTAGGA 6660
Db 6601 TTAGGTGAGGTTGAAGATGATGGGAGGTCTACACAGACGGAGCAACCATGCCAAGTAGGA 6660
QY 6661 GAGTATAGGCATACTGGGAGATTAGAAAATTAATTTACTGTACCTTAAACCTGAGTTTCCGT 6720
Db 6661 GAGTATAGGCATACTGGGAGATTAGAAAATTAATTTACTGTACCTTAAACCTGAGTTTCCGT 6720
QY 6721 AGCTATCACTCACCAATTTATGCATTTCTACCCCTGAACATCTGTGTGTAGGGAAGA 6780
Db 6721 AGCTATCACTCACCAATTTATGCATTTCTACCCCTGAACATCTGTGTGTAGGGAAGA 6780
QY 6781 GAATCAGAAAAGCCAGCTCATACAGAGTCCAAAGGCTCTTTGGGATATTTGGGTTATGA 6840
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QY 6841 TCACTGGGGTGTCTATTGAAGGATCCTAAGAAAGAGGACCACCATCTCCCTTATATGGTG 6900
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QY 6901 AATGTGTTGTTAAGAAGTTAGATGAGAGGTGAGGAGACCAAGTTAGAAAAGCCAAATAAGCAT 6960
Db 6901 AATGTGTTGTTAAGAAGTTAGATGAGAGGTGAGGAGACCAAGTTAGAAAAGCCAAATAAGCAT 6960
QY 6961 TTCCAGATGAGATAATGGTCTTGAATCCATAGTCCCGAGGTCTAAATTGAGATGG 7020
Db 6961 TTCCAGATGAGATAATGGTCTTGAATCCATAGTCCCGAGGTCTAAATTGAGATGG 7020
QY 7021 GTGAATGAGGAAAATAAGAAAGAGAGAGGCAAGATGGTGCCTAGGTTTGTGATGCCT 7080
Db 7021 GTGAATGAGGAAAATAAGAAAGAGAGAGGCAAGATGGTGCCTAGGTTTGTGATGCCT 7080
QY 7081 CTTTCTGGGTCTCTTGTCTCCACAGGAGGCCATGGGCACTACGCTCTAGCTGAACG 7140
Db 7081 CTTTCTGGGTCTCTTGTCTCCACAGGAGGCCATGGGCACTACGCTCTAGCTGAACG 7140
QY 7141 TGAGTGACACCCAGCTTCAGACTCTCTGTTGGGAAGAGAGCAAAACCTAGAGACTCAAGA 7200
Db 7141 TGAGTGACACCCAGCTTCAGACTCTCTGTTGGGAAGAGAGCAAAACCTAGAGACTCAAGA 7200
QY 7201 GGGAGTGCATTTATGAGCTCTTCATGTTTACAGGAGAGTTGAACCTTAAACATAGAATTT 7260
Db 7201 GGGAGTGCATTTATGAGCTCTTCATGTTTACAGGAGAGTTGAACCTTAAACATAGAATTT 7260
QY 7261 GCCTGACGAACCTCTGATTTTACGCTTCTGTGTTTCTTCCCTCAAAAAGATTTCCCCAT 7320

Db	7261	GCCTGACGAACCTCCTTGATTTTACCCCTTCTCTGTTTCATTTTCCCTCAAAAAGATTTCCCAT	7320
Qy	7321	TTAGGTTTCTGAGTTCCTGTCATGCCGCTGATCCCTAGCTGTGACCTCTCCCTCGGAACCTG	7380
Db	7321	TTAGGTTTCTGAGTTCCTGTCATGCCGCTGATCCCTAGCTGTGACCTCTCCCTCGGAACCTG	7380
Qy	7381	TCTCTCATGAACCTCAAGCTGTCATGAGAGCTTCCTTCATTTTCCCTCCGTCACCTCAGAG	7440
Db	7381	TCTCTCATGAACCTCAAGCTGTCATGAGAGCTTCCTTCATTTTCCCTCCGTCACCTCAGAG	7440
Qy	7441	ACATACACCTATGTCATTTTCCATTTTGGAGAGGACTCCCTTAAATTTGGGGGA	7500
Db	7441	ACATACACCTATGTCATTTTCCATTTTGGAGAGGACTCCCTTAAATTTGGGGGA	7500
Qy	7501	CTTACATGATTCATTTTAAACATCTGAGAAAGCTTTGAACCCCTGGGACGTGGCTAGTCAT	7560
Db	7501	CTTACATGATTCATTTTAAACATCTGAGAAAGCTTTGAACCCCTGGGACGTGGCTAGTCAT	7560
Qy	7561	AACCTTACCAGATTTTACACATGTCATGTCATTTTCTGGACCCGTTCACCTTTTCCCT	7620
Db	7561	AACCTTACCAGATTTTACACATGTCATGTCATTTTCTGGACCCGTTCACCTTTTCCCT	7620
Qy	7621	TTGAATCCTCTCTCTGTTTACCAGTAACCTCATCTGTACCAAGCCTTGGGATTTCTTC	7680
Db	7621	TTGAATCCTCTCTCTGTTTACCAGTAACCTCATCTGTACCAAGCCTTGGGATTTCTTC	7680
Qy	7681	CATCTGATTTGATGTGAGTTGTCACAGCTATGAAGCCTGTACACTGCACGAATGGAAGAG	7740
Db	7681	CATCTGATTTGATGTGAGTTGTCACAGCTATGAAGCCTGTACACTGCACGAATGGAAGAG	7740
Qy	7741	GCACCTGTCCAGAAAAGCATATGCGCTATCTGTGGGTAGTATGATGGGTGTTTTAGC	7800
Db	7741	GCACCTGTCCAGAAAAGCATATGCGCTATCTGTGGGTAGTATGATGGGTGTTTTAGC	7800
Qy	7801	AGGTAGGAGGCAAAATATCTTGAAGGGGTGTGAAGAGGTGTTTTTCTAATTTGGCATGA	7860
Db	7801	AGGTAGGAGGCAAAATATCTTGAAGGGGTGTGAAGAGGTGTTTTTCTAATTTGGCATGA	7860
Qy	7861	AGGTGTCATACAGATTTGCAAAAGTTTAAATGGTGCCTTCATTTGGGATGTACTTASTAT	7920
Db	7861	AGGTGTCATACAGATTTGCAAAAGTTTAAATGGTGCCTTCATTTGGGATGTACTTASTAT	7920
Qy	7921	TCCAGACCTGAAGATCACAAATTAATTTTACCTGGTCTCTCCTGTTTCGATTAATGAAA	7980
Db	7921	TCCAGACCTGAAGATCACAAATTAATTTTACCTGGTCTCTCCTGTTTCGATTAATGAAA	7980
Qy	7981	ATTATGATAAGGATGATAAAGCACTTACTTCGTGTCGGACTCTTCTGAGCACCTACTTA	8040
Db	7981	ATTATGATAAGGATGATAAAGCACTTACTTCGTGTCGGACTCTTCTGAGCACCTACTTA	8040
Qy	8041	CATGCATTTACTGCATGCACTTCTTACAAATTAATTTCTATGAGATAGGTACTAATATCCC	8100
Db	8041	CATGCATTTACTGCATGCACTTCTTACAAATTAATTTCTATGAGATAGGTACTAATATCCC	8100
Qy	8101	TTCTTTTTTAAATGAAGAAAGTGAAGTGAAGCGGACAGGTGCTCAGCGCTGTAATCCC	8160
Db	8101	TTCTTTTTTAAATGAAGAAAGTGAAGTGAAGCGGACAGGTGCTCAGCGCTGTAATCCC	8160
Qy	8161	AGCACTTTGGAGGCCAAAGCGGTGGATCACAGGTCAGAGGTCAGAGACCATCTCGC	8220
Db	8161	AGCACTTTGGAGGCCAAAGCGGTGGATCACAGGTCAGAGGTCAGAGACCATCTCGC	8220
Qy	8221	TAAACATGGTGAACCCCATCTCTAATTAATAATACAAAATTAAGTGGGGGTGGTGGCAG	8280
Db	8221	TAAACATGGTGAACCCCATCTCTAATTAATAATACAAAATTAAGTGGGGGTGGTGGCAG	8280
Qy	8281	ACGCGTGTAGTCCCAGCTACTCGGAAGGCTGAGGAGGAGATGGGATGAACCCAGGAGG	8340
Db	8281	ACGCGTGTAGTCCCAGCTACTCGGAAGGCTGAGGAGGAGATGGGATGAACCCAGGAGG	8340
Qy	8341	CAGAGCTTGAGTGGCCGAGTTTGGCCCACTGCACCTCCAGCCTAGGTGACAGAGTGAGA	8400
Db	8341	CAGAGCTTGAGTGGCCGAGTTTGGCCCACTGCACCTCCAGCCTAGGTGACAGAGTGAGA	8400
Qy	8401	CTCCATCTCAAAAAATAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATA	8460
Db	8401	CTCCATCTCAAAAAATAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATA	8460
Qy	8461	TAGAGTATCTCATAGTTTGTCTAGTATAGAAACAGGTTTCAAACTCAGTCAATCTGACCG	8520
Db	8461	TAGAGTATCTCATAGTTTGTCTAGTATAGAAACAGGTTTCAAACTCAGTCAATCTGACCG	8520
Qy	8521	TTTGATACATCTCAGACACCACTACATTCAGTAGTATAGATGCCCTAGAAATAAATAGAAA	8580
Db	8521	TTTGATACATCTCAGACACCACTACATTCAGTAGTATAGATGCCCTAGAAATAAATAGAAA	8580
Qy	8581	GGAAGGAGATGGCT	8640
Db	8581	GGAAGGAGATGGCT	8640
Qy	8641	GGAAGGAGACACAGAAAACAAACCAACCTGATCCCTCAGCTGCATGTTTCCCTTTAAAGTC	8700
Db	8641	GGAAGGAGACACAGAAAACAAACCAACCTGATCCCTCAGCTGCATGTTTCCCTTTAAAGTC	8700
Qy	8701	CCTGAAGGAAGTCTCTGGAATCTGACTCCCTTGCTCTCTCTCTCTCTCTCTCTCTCTCT	8760
Db	8701	CCTGAAGGAAGTCTCTGGAATCTGACTCCCTTGCTCTCTCTCTCTCTCTCTCTCTCTCT	8760
Qy	8761	TTTCTTTGGACCCCTACGCAAGGACTGTAAATTTGGTGGGACAGCTAGTGGCCCTGCTGGGC	8820
Db	8761	TTTCTTTGGACCCCTACGCAAGGACTGTAAATTTGGTGGGACAGCTAGTGGCCCTGCTGGGC	8820
Qy	8821	TTTCACACAGCGTGTCTCTCCCTAGGCGAGTCCCTCTGAGGACAGTCTGGTGGTATTTTC	8880
Db	8821	TTTCACACAGCGTGTCTCTCCCTAGGCGAGTCCCTCTGAGGACAGTCTGGTGGTATTTTC	8880
Qy	8881	CCTCAATGAAGTGGAGTAAAGTCTCTCAATTTTGAGATGGTATTAATGGAAGCCACCACTG	8940
Db	8881	CCTCAATGAAGTGGAGTAAAGTCTCTCAATTTTGAGATGGTATTAATGGAAGCCACCACTG	8940
Qy	8941	GCTTAGAGGATCCCAGGTCTCTCCATGGAGCCACTTGGGGTTCGGGTGCACATTAATAAAA	9000
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; Patent No. 6228594
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect Version 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,444A
; FILING DATE: 14-Feb-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/652,265
; FILING DATE: 23-May-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,673
; FILING DATE: 16-Apr-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,912
; FILING DATE: 04-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0088-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 5:
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
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for 24d1(G) allele (SEQ ID NO:20)"
FEATURE:

NAME/KEY: allele
LOCATION: replace(3872, "g")
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OTHER INFORMATION: /label= 24d2

US-09-503-444A-5

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 4381 TGGCCCAACCAAGCTGGAGTGGGAAGGACAGATTCGGGCCAGGACAGAGGGCTTAC 4440
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Db 4501 GACCAACAAGGTATGTTGGAAACACACACTTCTGCCCTATATCTACTGGCAGAGTGGAGG 4560
QY 4561 AGTTGCAGGGCAGGAAATCCCTGGTTGGAGTTTCAGAGTGGGCTGAGGCTGTGGCTTC 4620
Db 4561 AGTTGCAGGGCAGGAAATCCCTGGTTGGAGTTTCAGAGTGGGCTGAGGCTGTGGCTTC 4620
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Db 4621 TCCAAATTCGGAAGGACTTTCTCAATCCTAGAGTCTCTACCTTATATTTAGATGTA 4680
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Db 4681 TGAGACAGCCACAAAGTCATGGGTTTAAATTTCTTCTCCATGCATATGGCTCAAAAGGAA 4740
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Db 4801 AAATTCAGAAATGTCAGGCCGGGACCGGTGGCTACCCCTGTAAATCCAGCAGCTTTGGG 4860
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Db 4861 AGGCCAGGGGGTGTCAAGGTCAGGAGTTTGAGACCCAGCCTGACCAACATGGTCAA 4920
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Db 4921 ACCCGTCTCTAAAAAATACAAAAATTAGCTGGTCACAGTCATGGTCACAGTCATGGTCCA 4980
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Db 5461 ACACAAAATGTTGCTCC 5520
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Db 5581 CTCATC 5640
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